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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
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     1100554
1100554
1100554
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   512.8
511.2
501.6
509.6
60.8
487
460.8
454.4
448
444.4
4406.4
4406.4
392.8
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7:
8:
9:
110:
112:
113:
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516
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11046.851 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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gb_est4:*
gb_est5:*
gb_est5:*
gb_htc::
gb_htc::
gb_est2:*
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BM863356 mgcm006x0
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BM863315 mgcm006xE
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BM863140 mgcm007xE
BM863710 mgcm007xE
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BM863358 mgcm005xH
BM863359 mgcm005xJ
BM863359 mgcm005xJ
BM86337 mgcm006xA
BM863472 mgcm010xJ
BM864472 mgcm010xJ
BM864473 mgcm006xC
BM863374 mgcm006xC
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BM863394 mgcm006xC
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BM863196 mgcm001xJ
BM861796 mgcm001xJ
BM861796 mgcm001xJ
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57	57.2	71.8	79.2	86.8	91.4	105	107	112.2	124.2	181.6	213.4	217	230.8	232.2	237	239.6	257	257.8	260	260	267	292.8	298.6	301.4	303.8
11.0	11.1	13.9	15.3	16.8	17.7	20.3	20.7	21.7	24.1	35.2	41.4	42.1	44.7	45.0	45.9	46.4	49.8	50.0	50.4	50.4	51.7	56.7	57.9	58.4	58.9
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	AL053013 Drosophil	BM863872 mgcm007xL	CD028659 mgcm006xG	DN476575 altr207xo	BE188286 PSI61R3 I	CK906746 rhzma0_00	BP100008 BP100008	BG280255 c2b06np.r	BE188285 PSI61F In	CD276416 T143B0271	BM871833 mgns015xB	CD274144 T143B0403	BQ109916 VD0100E09	CD275678 T143B0071	CD275940 T143B0156	CD273332 T143B0196	CD035120 mgmt018xL	BM863213 mgcm005xD	CD275905 T143B0122	CD275566 T143B0121	CD035038 mgmt018xH	CD036729 mgsu011xC	CD034317 mgmt015xP	BM861952 mgcm001xL	BM864053 mgcm008xM

ALIGNMENTS

RESULT 1

source	FEATURES								COMMENT	JOURNAL	TITLE		AUTHORS	Daggaga		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	BM863356
1619 /organism="Magnaporthe grisea" /mol_type="mRNA" /strain="Guy11" /db_xref="taxon:148305" /clone="mgcm065x003" /sex="Mat1-2 hermaphrodite"	Seq primer: T3. Location/Qualifiers	BACKWARD: T7 primer Plate: mgcm006 row: O column: 03	PCR PRimers FORWARD: T3 primer	dehydratase >gi 1127197 pdb 1STD 367 e-101	Chromatogram file of this sequence is available, see contact	Fax: 979 845 6483 Email: d-ebbole@tamu.edu	Peterson Bldg, MS2132, College Station, TX 77843-2132, USA	Department of Fiant Fathology & Microbiology	On Mar 7, 2002 this sequence version replaced gi:19231038.	grisea Unpublished (2002)	Expressed sequence tags from the rice blast fungus, Magnaporthe	Bhatterai, K. and Dean, R.A.	Ebbole.D.J. Yuan.J. Thomas.T.L. Bobrowicz.P. Lu.G.	Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		Magnaporthe grisea (anamorph: Pyricularia grisea)		RM863366.2 GT:30391591	BARE3356		BM863356 619 bp mRNA linear EST 06-MAY-2003	

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RESULT 2
BM864194
                                                                                                                                                         VERSION
KEYWORDS
                                                             REFERENCE
                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                         DEFINITION
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                                          AUTHORS
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                                                                                                                                                                                              657 bp mRNA linear EST 06-MAY-2003 mgcm008xJ12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xJ12 5', mRNA sequence.
BM864194
                                                                                                                  Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G. Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Ma
                                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 657)
                                                                                                                                                                               BM864194.2
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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                                                                                                                                                                             GI:30390885
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Pred. No. 4.3e-115;
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fungus, Magnaporthe
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Query Match
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Peterson Bldg, MS2132, College Station, TX 77843-
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@ramu.edu
Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|SC
dehydratase >gi|1127197|pdb|1STD|...365 e-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
On Mar 7, 2002 this
Contact: Ebbole DJ
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Seq primer: T3.
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                    GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
                                                                                                      ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                                                                                                                                                        CTCCGCACGCACGTTCATCGGCGCGCGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC
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/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptSK-; Site_1: EcoRI, Site_2:
XhoI; Unidirectional cloning. EcoRI—side has T3 prīmer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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Pred. No. 7.6e-115;
0; Mismatches 3;
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                                        Query Match
Best Local Similarity
Matches 513; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ
Department of Plant Pathology & Microbiology Texas & M. University
Peterson Bldg, MS2132, College Station, TX 77 Tel: 979 845 483
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM863315

mgcm006xE21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xE21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) spjp56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...364 e-100
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BM863315
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    ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
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                                          Conservative
                                                                                                                                        /cell type="mycellum"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptsK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h. room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredphrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:148305"
/clone="mgcm006xE21"
/sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain="Guy11"
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                                        Score 511.2; DB 3;
Pred. No. 1.1e-114;
0; Mismatches 3;
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BM863340
                                                     Plate: mgcm006 row:
Seq primer: T3.
                                                                                                                                                                                                                                            Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 7 Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
On Mar 7, 2002 thi
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Magnaporthe grisea
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EST.
                                                                                                 FORWARD: T3 primer BACKWARD: T7 prime
                                                                                                                                                             Bmail: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scy
dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99
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                                      Location/Qualifiers
organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                   2002 this sequence version replaced
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Magnaporthe
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380 300 320 240 260

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SOURCE
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                                                                               mgcm006xF04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xF04 5', mRNA sequence.
BM863546
BM863546.2 GI:30391437
EST.
EST.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                             GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGGCGAGTTCGACTTTGACAGG
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/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note=""Vector: BBluescriptSK-; Site 1: ECRI, Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h. room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/strain="Guy11"
/db_xref="taxon:148305"
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Pred. No. 2.6e-114;
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Expressed sequence tags from the rice blast fungus, Mag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|St
dehydratase >gi|1127197|pdb|15TD|. . . 322 2e-87
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Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Mar 7, 2002 this
Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 593)
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ATCGGCTACCACCAGCTGCGCGCCCCGCACCAGAGGTACAAGGACCCACCATGAAGGAG
                                                                                                                                                                           ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
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                                                                                                        CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC
                                                                                                                                                   CTCCGCACGCACTTCATCGCCGCACGCGCTGAGAGAAGGTGTCCGAGGACGAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="mycelium"
/clone lib="Magnaporrhe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporrhe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporrhe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptSK-; Site_1: EcoRI_side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 9910.9 and trimmed according to phd files (0.05) and for vector seqs."
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/mol_type="mRNA"
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/sex="Mat1-2 hermaphrodite"
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Pred. No. 9.1e-109;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ Department of Plant Pathology & Microbiology Department Of Plant Pathology & Microbiology Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD| . . . 302 3e-87
PCR PRimers
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Tel: 979 845 4831
Fax: 979 845 6483
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: T3.
       /sex="Matl-2 hermaphrodite"
/cell type="mycellum"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm, bequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:148305"
/clone="mgcm008xD02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="Guy11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Magnaporthe grisea"
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             GATCTTTGAGGACGGACGGAGACCTTTGGCGACAAA 516
                                               GTTCTGAAGTTCATGAGCCTTTACGCCCGACAGTCGCTGGCGAGGTTCGAGTTTGACCG
                                                            GTCTGGAAGTTCGCCGGCC-TCAAGCCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAG
                                                                                                           GTCACCATGAAGGGCCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
                                                                                                                                          ATCGGCTACCAGCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
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                                                                                           GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
                                                                                                                                                                ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
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Pred. No. 3.8
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RESULT 7 BM863710 LOCUS DEFINITION BM863710 571 bp mRNA linear EST 06-MAY-2003 mgcm007xE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm007xE24 5', mRNA sequence. BM863710.2 GI:30391295

ACCESSION VERSION KEYWORDS EST.

SOURCE ORGANISM

Magnaporthe grisea (anamorph: Pyricularia grisea)

REFERENCE AUTHORS Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Bhatterai, K. and Dean, R.A. Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; (bases 1 to 571) Lu, G

Expressed sequence tags from the rice blast fungus, Magnaporthe

TITLE

COMMENT

Unpublished (2002)
On Mar 7, 2002 this sequence v
Contact: Ebbole DJ
Department of Plant Pathology
Texas A&M University 2002 this sequence version replaced gi:19231392

Peterson Bldg, MS2132, Tel: 979 845 4831 Fax: 979 845 6483 College Station, TX 77843-2132,

& Microbiology

Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp[P56221|SCYD_MAGGR Scytalone
person;Best nr hit (April. 22, 2003) sp[P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...336 1e-91 PCR PRimers

BACKWARD: T7 primer primer

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RESULT 8
BM864467
SOURCE
ORGANISM
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Seq pri
                                                                             {\tt mgcm010xH12f.b} Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone {\tt mgcm010xH12~5'}, {\tt mRNA} sequence.
Magnaporthe Magnaporthe
                                   EST.
                                                                grisea cDNA clone
BM864467
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                                                                                                                                                                                                                      GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
                                                                                                                                                                                                                                                                                GTCACCATGAAGGGCCCACCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
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/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptsK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/strain="Guy11"
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                (anamorph: Pyricularia grisea)
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Pred. No. 2.5e-102;
0; Mismatches 12;
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Contact: Ebbole DJ
Department of Plant Pathology
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Seq prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
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BACKWARD: T7 prime:
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                                                  CTCCGCACGCACTTCATCCGCCGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTC
                                                                                                ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
                                                                                                                                                                                                                                                                                             ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
   ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                CTCCGCACGCACTTCATCGGCGCCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="mgcm010xH12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA
/strain="Guy11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Magnaporthe grisea"
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97.0%;
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Pred. No. 9.3e-101;
0; Mismatches 12;
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384 240

300 444

360

120

204 60

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Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
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                                                                                                                                                                                    /cell type="mycellum"
/cell type="mycellum"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredbrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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Indels
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Gaps
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|St
dehydratase >gi|1127197|pdb|1STD|... 272 3e-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson Bldg, MS2132, College
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: mgcm006 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Plant Pathology & Microbiology
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grisea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Bhatterai, K. and Dean, R.A.
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1 (bases 1 to 602)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer: T3.
           /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                              /organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:148305"
/clone="mgcm006xH04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                     /sex="Mati-2 hermaphrodite"
/cell_type="mycelium"
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Best Local Similarity
Matches 477; Conserv
                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    574
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                                                      Texas A&M University
Peterson Bldg, MS2132, Col
Tel: 979 845 4813
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
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                                                                                                                              Unpublished (2002)
on Mar 7, 2002 this sequence version replace.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                               Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Mag
                                                                                                                                                                                                                                                                                                                                               BM863209.2 GI:30391705
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                                                                                                                                                                                                                                                      (bases 1 to 523)
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Pred. No. 3.4e-99;
                                                                                                     College
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RESULT 11
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                                                                      DEFINITION
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                                       BM863639
486 bp mRNA linear EST 06-MAY-2003 mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm007xG13 5', mRNA sequence.

BM863639
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Plate: mgcm005
                             BM863639.2
                                                                                                                                                                     GTCTGGAAGTTCGCCGGC 438
                                                                                                                                                                                                                             GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
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                                                                                                                                                      GTCTGGAAGTTCGCCGGC 523
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/sex="Mat1-2 hermaphredite"
/cell_type="mycelium"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Inide has T3 primer and predominantly 5 reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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grisea
                             GI:30391353
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99.5%;
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Pred. No. 5.8e-96;
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Query Match
Best Local S
Matches 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: T7 primer Plate: mgcm007 row: G Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
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Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
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1 (bases 1 to 486)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbol@etamu.edu
Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|sc
dehydratase >gi|1127197|pdb|1STD|. . . 293 5e-79
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                           CTCCGCACGCAGCACTTCATCGGCGGCACGCCACGCGCTGGGAGAGGTGTCCGAGGACGAGGTC
                                                                                                                                ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAGCAGCAGTGCTGGGCGACCCCACC
                                                                                                                                                                                                                                               ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
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                                                                                                       CTCCGCACGCAGCATTCATCGGCGGCACGCGCTGGGAAAGGTGTCCGAGGACGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="mycelium"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptSK-; Site_1: EcoRI, Site_2:
XhoI; Unidirectional cloning. EcoRI—side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed
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/clone="mgcm007xG13"
/sex="Mat1-2 hermaphrodite"
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98.6%;
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Pred. No. 6.4e-93;
0; Mismatches 6;
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RESULT 12
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AUTHORS
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19232154.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) sp[p56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 6483

Fax: 979 845 6483
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Ebbole,D.J., Yuan,J., Thomas,T.L.,
Bhatterai,K. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm010 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM864472.2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: d-ebbole@tamu.edu
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                                                             /cell_type="mycelium"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptSK; Site_1: EcoRI, Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                             /organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
                                                                                                                                                                                                                                                                                                           /sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                           /clone="mgcm010xJ04"
                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:148305"
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78.8%;
97.0%;
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Score 406.4; DB 3
Pred. No. 5.6e-89;
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GTCTGGAAGTTCGCCGGC 438
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                                                                                                               GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
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                                                                            GTCACCATGAAGGGCCACGCCCACTCGCAAAAACCT--CATTGGACAAGAAGATCGACGGC
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On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ Department of Plant Pathology & Microbiology Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Magnaporthe grisea
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe mgap007xA05f.b Magnaporthe grisea grisea cDNA clone mgap007xA05 5', BM864820 Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|SC
dehydratase >gi|1127197|pdb|13TD|...271 1e-71 Texas A&M University Peterson Bldg, MS2132, Tel: 979 845 4831 Fax: 979 845 6483 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Mag FORWARD: T3
BACKWARD: T PCR PRimers Unpublished (2002) BM864820.2 GI:30390364 Plate: mgap007 primer: T3. (bases 1 to 781) /organism="Magnaporthe
/mol_type="mRNA" Location/Qualifiers T7 primer primer Þ College 781 bp Station, grisea" rice blast fungus, Magnaporthe mRNA linear EST 06-MAY-2003 Ap Uni-Zap XR Library Magnaporthe mRNA sequence. replaced TX 77843-2132, Sordariomycetes; gi:19232502 SCYD_MAGGR Scytalone see contact

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RESULT 14
BM863357
                                                                                                                 ACCESSION
VERSION
 REFERENCE
                                                         SOURCE
ORGANISM
                                                                                                                                                                        DEFINITION
                                                                                             CEYWORDS
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Best Local Similarity 91.1
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 530)
                                                                                                                                                    {\tt mgcm006x005f.b} Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone {\tt mgcm006x005~5'}, {\tt mRNA} sequence.
                                                         Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                   BM863357.1 GI:19231039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell type="Appressorium"
/clone lib="Magnaporthe grisea Ap Uni-Zap XR Library"
/clone lib="Magnaporthe grisea Ap Uni-Zap XR Library"
/note="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Appressorium library. Conidia were germ inated on an inductive surface for 5-8 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was attimed according to the alignment, otherwise sequence guality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector
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/clone="mgap007xA05"
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91.1%;
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Texas A&M University
Peterson Bldg, MS2132, College Station, TX 7
Tel: 979 845 4831
Fax: 979 845 6483
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Chromatogram file of this sequence is available, see conta
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR
dehydratase >gi|1127197|pdb|1STD|... 276 le-73
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Bhatterai,K. and Dean,R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed sequence tags from the rice blast fungus, Magnaporthe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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                                                                           ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                                                                                                                                                                                                                                                           ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 396
                                                                                                                                              CTCCGCACGCACTTCATCGGCGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC
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                                                                                                                                                                                                                                              Conservative
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//clone="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning: EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 xpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 xpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/cell_type="mycelium"
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/strain="Guy11"
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/clone="mgcm006x005"
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99.7%;
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Pred. No. 4.8e-86;
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Qy J	B 8	Query Mat Best Loca Matches	ORIGIN .	FEATURES SOUICE	TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Db . RESULT 15 BM863374 LOCUS DEFINITION
61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120 	1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60	ch 76.1%; Score 392.8; DB 3; Length 510; al Similarity 99.5%; Pred. No. 1.2e-85; 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	/ox//ox//ox//ox//ox//ox//ox//ox//ox//ox	Fax: 979 845 6483 Email: d-ebbole@tamu.edu Chromatogram file of this sequence is available, see contact Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) sp F56221 SCYD_MAGGR Scytalone dehydratase >gi 1127197 pdb 1STD 276 1e-73 PCR PRimers FORWARD: T3 primer BACKWARD: T7 primer BACKWARD: T7 primer Plate: mgcm006 row: C column: 10 Seg primer: T3. Location/Qualifiers 1510	Expressed sequence tags from the rice blast fungus, Magnaporthe grisea Unpublished (2002) On Mar 7, 2002 this sequence version replaced gi:19231056. Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel: 979 845 4831	grisea CDNA Clone mgcm006XCl0 5', mRNA sequence. BM663374.2 GI:30391576 EST. Magnaporthe grisea (anamorph: Pyricularia grisea) Magnaporthe grisea (Enamorph: Pyricularia grisea) Magnaporthe grisea (Enamorph: Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 510) Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.	CACGCCCACTCGGCAAA

443 GICALMANGGOLUANGCILANTINGGEAAAANCIT 4/8	7# £	-
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361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 396	Оу 361	_
ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG	Db 383	н
301 ATCGGCTACCAGCTGCGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG	Оу 301	\sim
323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGACGAGGTC 382	Db 323	_
241 CTCCGCACGCAGCACTTCATCGGCGCGCACGCGCTGGGAGAAGGTGTCCGAGGACGACGACGTC	Оу 241	\sim
ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCA	Db 263	_
181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCA	Qу 181	\sim
203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCT	Db 203	-
121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCT	Оу 121	~

Search completed: December 4, 2006, 19:19:10 Job time : 2616 secs

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Result
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US-10-507-132-18
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60707, A
16567, A
52204, A
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ALIGNMENTS

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LENGTH: 516
TYPE: DNA
CORGANISM: Pyricularia of FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(516)
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Sequence 1, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: Koichiro KAKU et al.

TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

TITLE OF INVENTION: USAGRICULTURAL FUNGICIDAL AGENT

CURRENT FILLE REFERENCE: 1254-0258PUS1

CURRENT FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: JP 2002-66955

PRIOR RILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
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Best Local Similarity
Matches 516; Conserv
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Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHINO GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US/202-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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Best Local Similarity
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ORGANISM: Pyricularia
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                                             ATCGGCTACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
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Pred. No. 1.6e-112;
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Best Local (
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Similarity 99.8%;
15; Conservative
                     ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KOICHITON: GENE CODING POR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: GENE CODING POR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT FALLOATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 600
TYPE: DNA
ORGANISM: Pyricularia oryzae
US-10-507-132-13
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Pred. No. 1.7e-112;
0; Mismatches 1;
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Sequence 15, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHIYO KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REPERENCE: 1254-0258PUS1

CURRENT APPLICATION NUMBER: US/10/507,132
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Best Local Similarity
Matches 515; Conserv
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Publication No. US20060223136A1
GENERAL INFORMATION:
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SEQ ID NO 16
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TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-02589US1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
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TYPE: DNA
ORGANISM: Pyricularia oryzae
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CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
SEQ ID NO 15
IENGTH: 538
TYPE: DNA
ORGANISM: Pyricularia oryzae
US-10-507-132-15
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US-10-507-132-14
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US-10-507-132-14
                                                    Sequence 14, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
TITLE OF INVENTION: NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF EEQ ID NOS: 19
SOFTMARE: Patentin Ver. 2.1
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           LENGTH: 545
TYPE: DNA
ORGANISM: Pyricularia oryzae
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Pred. No. 3e-110;
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Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHINFORMATION:
APPLICANT: KOICHINFORMATION:
APPLICANT: KOICHINFORMATION:
AGRICULTURAL FUNGICIDAL AGENT
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
TITLE REFERENCE: 1254-0258PUS1
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT PILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOCTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 729
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  ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCGTATGTTCCGCCCTGCCAT
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                                                                                                                                                      73.2%; Score 377.8; DB 6
84.5%; Pred. No. 3.6e-80;
vative 0; Mismatches 2
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Pred. No. 3e-110;
0; Mismatches 2;
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publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: KOIGHIYO KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

FILE REFERENCE: 1254-0258US1

CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: JP 2002-66955

PRIOR FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 732

TYPE: DNA

COGANISM: Pyricularia oryzae

US-10-507-132-17
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                                                                                                                                      GGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGA 495
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                                                                                                                                                                                                                     CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCTCAAGCCCGACATCCGCTGGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGC 375
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Pred. No. 3.2e-79;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                      Length
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Gaps

191

287 141 227

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GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION UMBER: JP 2002-203269

PRIOR APPLICATION UMBER: JP 2002-383870

PRIOR APPLICATION UMBER: JP 2002-383870

PRIOR APPLICATION UMBER: JP 2002-383870

PRIOR FILING DATE: 2002-12-11

NUMBER: OF SEQ ID NOS: 56791

SOPTWARE: Patentin Ver. 2.1

LENGTH: 3067
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US-10-449-902-18394
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Best Local Similarity
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Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                        -10-449-902-18394
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: OTYZA BATIVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK068793
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                 350
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                                                                                                                                                                                                                                                                                             171;
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ATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTG 318
                                                                                                                                      ATCTTCTCCTCCTACTGCGCCAGCGCCAACCTCAGGAAGGCCGTCGAGGCCTTCGACGTC
                                                                                                                                                                          GCCGTCCGCACCATGAACAAGGAGGGCGGCGCCGCCTCGTCACCGTCGCCACCTTCGCCTCC
                                                                                                                                                                                                                                                     GCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTG
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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-383870

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 13052
LENGTH: 3161
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION UNMERR: AK110400
DATABASE ENTRY DATE: 2001-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13052, Application US/10449902
Publication No. US20060123505A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                      404
                                                            446
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ACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGC 438
                                                                                              ACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGT
                                                                                                                                                                          TGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGCGTCCCGCACCAGAGGTACAAGG
                                                                                                                                                                                                               CGCGCGGGATGGGCATCGTCGGCGGGAAGGGCGGCGGCGGCGGGAGCAGCGACTCGG
                                                                                                                                                                                                                                                                                                                               ACTCCGGGCTCTGCACCAAGGGCGGCGACGTGTGCTTCGTCAGCATCGACGCCAGCGGGA
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                                                            TCAGCGTCGAGCAGGTGGTGCCAACCTCGTCGACGCCAACATCATCGGCAAGGGCTGCT
                                                                                                                                      AGTCCGGCGGCGA----CCTGGCGTGGCCGTGGCAGTTCACGCCGTTCCAGAAGCTGAGCT
                                                                                                                                                                                                                                                   TecTegeceaccccaccrocecacecaecaecactroarcegececacececregaeaaaee
                                                                                                                                                                                                                                                                                           TCGCGCTGCTGGTGACGGCGACGGTGGCGATGGTGCTGGGCATGGTCGGGATCCTACGGG
                                                                                                                                                                                                                                                                                                                                                                      GGCCGGTGATGAGCGCCGACGAGGAGGAGGTGCAGCGGATGCACCGGCTCAAGCTCGCCA
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47.3%;
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Pred. No. 0.0097;
0; Mismatches 205;
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Gaps

223

564 283

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CCGGCGTGGTGTACCGCGTCGGCCTCGACACCGGC 352

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RESULT 12
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; LOCATION: (1)..(750)
; OTHER INFORMATION: Ortholog
; OTHER INFORMATION: as cited
US-11-056-355B-18159
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US-11-056-355B-18159
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 18159
LENGTH: 760
TYPE: DNA
COCANICAN: Gas mayor sinhen mayor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1). (760)
OTHER INFORMATION: Ortholog
OTHER INFORMATION: as cited
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LOCATION: (1) (760)
OTHER INFORMATION: Ortholog
OTHER INFORMATION: as cited
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LOCATION: (1)..(760)
OTHER INFORMATION: Ceres
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NO 1394
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NO 56088
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                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MONSANTO TECHNOLOGY,
APPLICANT: MCLAIRD, Paul L.
                                                                                                                                                                                                                                                               Sequence 7648, Application US/11218305 Publication No. US20060141495A1
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Best Local :
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Corn.
FILE REFERENCE: 38-21 (53660)B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
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PRIOR FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/471,423
PRIOR FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: 60/418,467
PRIOR FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PROTEASES, NUCLEIC ACIDS ENCODING TITLE OF INVENTION: AND METHODS FOR MAKING AND USING FILE REFERENCE: 564462004100

CURRENT APPLICATION NUMBER: US/10/530,643

CURRENT FILING DATE: 2006-04-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Bacteria
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Local Similarity 48.7%;
nes 134; Conservative
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BARTON, Nelson R.
STEGE, Justin T.
ABOUSHADI, Nahla M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCCLURE, Amy
SUN, May
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Pred. No. 0.02;
0; Mismatches 141;
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NUMBER OF SEQ ID NOS: 25043

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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oxiented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT APPLICATION NUMBER: US/2002-203269

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID MOS: 56791

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 23999

LENGTH: 749
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US-10-449-902-23999
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Best Local Sim:
Matches 150;
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SEQ ID NO 7648
LENGTH: 1000
TYPE: DNA
ORGANISM: Zea mays
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Best Local (
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                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK09:
DATABASE ENTRY DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                             GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGA 359
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CGGCACCAAGCGCCTCTGCCACATCCGCGGCAAGATGCACAAGAAGGTGTGGATCGCCGC
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48.6%;
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Pred. No. 0.021;
0; Mismatches 143;
                                                                                                                                             Score 48; DB 6;
Pred. No. 0.037;
0; Mismatches 1:
                                                                                                                                                 170;
                                                                                                                                                                                 Length 749;
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Search completed: December Job time : 221 secs
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US-10-953-349-26476
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 26476
LENGTH: 750
TYPE: DNA
TORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 150; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                      GAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                        CCCCACCCTCCGCACGCACCTTCATCGGCGCACGCCTGGGAGAAGGTGTCCGAGGA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTACGCGCAGGTGACGCGGATGCTCGGCAACGGGCGCTGCGAGGCCATCTGCGTCGA
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                                                                          CATCCAGTTCGAGGACGAGG
                                                                                                          TGACAGGATCTTTGAGGACG 493
                                                                                                                                                                                                                                                                                                                              CGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCAT
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                                                                                                                                            CCGCCTCAACGAGGGCGTCGACGTCGACGGCCCCGAGGAGGGCGAGGGCGACAGCGACTA
                                                                                                                                                                                CGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTT
                                                                                                                                                                                                                                                                                            CGGGGACATCGTCCTCGTCGGCCTCCGCGACTACCAGGACGACAAGGCCGACGTCATCCT
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                    4, 2006, 19:11:46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 6; Length 750; Pred. No. 0.037;
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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Match Length DB
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| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
| JEMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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                                                                               Listing first 45 summaries
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7 US-10-156-761-1

2 US-10-478-943D-1

7 US-10-246-330-3

1 US-10-282-122A-30151

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1 US-10-425-114-29012

1 US-10-425-114-29012

1 US-10-425-114-29011

2 US-10-425-144-29011

2 US-10-425-144-29011

2 US-10-425-144-29011

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2 US-10-425-144-29011

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                    Sequence 3, Appli
Sequence 30151, A
Sequence 23119, A
Sequence 23119, A
Sequence 29012, A
Sequence 17854, A
Sequence 29011, A
Sequence 45, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 1768, A
Sequence 14768, A
Sequence 14768, A
Sequence 14768, A
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Sequence 27772, A	10067	e 29006,	28991,	17863,	Sequence 16556, A	17865,	437	Sequence 16569, A	41,		ce 14525,		429	75,	75,	4792	Sequence 82, Appl	e 82,	æ	e 4356,	e 10065,	e 100	e 4590,	e 16604,	e 6352,	Sequence 14248, A

ALIGNMENTS

US-10-156-761-6148

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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6148
LENGTH: 1479
TYPE: DNA
ORGANISM: Streptomyces avermitilis
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APPLICANT: IKEDA, HARUO
APPLICANT: ISTEAMA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                   US-10-156-761-6148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6148, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                        Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1479)
TACCTCTTCCGCTTCGAGGGCTTCGACGTGGTCGGCTCGTCCCCCGAGGCCCCTCGTCAAG
                                                                                                                             Conservative
                                                                                                                                           11.4%;
50.5%;
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                                                                                                                            Score 58.6; DB 7;
Pred. No. 7.3e-07;
0; Mismatches 139;
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Sequence 137,

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US-10-478-943D-1
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US-10-156-761-1
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APPLICANT: HATTORI, WASHAIRA
TITLE OF INVENTION: WASHAIRA
TITLE OF INVENTION: WOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILLING DATE: 2001-08-02
PRIOR FILLING DATE: 2001-08-02
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Best Local Similarity
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Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: a, t, c, -10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIR
APPLICANT: SHIBA, TADAYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 15109
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NAME/KEY: misc feature
LOCATION: (4187715)
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                                                                                  GTCGAGGTCGTCGACTTCATGACCATCGAGCGCTACTCGCA 7418899
                                                                                                                                                                                                                                    CCGCAGGAGGACCAGGCCCTCGCGGACGAGCTGCTGGCCGACCCCAAGGAGCGCGCCGAG
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                                                                                                                                                           CACCTGATGCTCGACCTGGGGCCCAACGATCTGGGGCGGGTCTGCGAGCCCGGTTCC
                                                                                                                                                                                                CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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ilarity 50.5%;
Conservative
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Pred. No. 2.9e-06;
0; Mismatches 139
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                                            ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-10-246-330-3
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US-10-246-330-3
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                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10246330
Publication No. US2003016030A1
GENERRAL INFORMATION:
APPLICANT: O'Toole, George A.
APPLICANT: Mah, Thien-Fah
TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
TITLE OF INVENTION: BIOFILM-SPECIFIC ANTIBIOTIC RESISTILE REFERENCE: 14537-002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10478943D
Publication No. US20060073574A1
GENERAL INFORMATION:
APPLICANT: University College Dublin, National University of Ireland
TITLE OF INVENTION: Engineered biosynthesis of novel polyenes
FILE REFERENCE: PC-1636US
                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/246,330
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,241
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3 SEQ ID NO 1
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           Query Match
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                                                                                                                                      LENGTH: 7407
TYPE: DNA
                                                                                                                     ORGANISM: Pseudomonas
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Local Similarity 47.5%;
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           Score
           53;
           DB
           7;
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                                                                                          PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/269,308
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                                                                       PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NO 30151
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Yamamoto, Ro
Forsyth, R.
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Malone, Cheryl
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                                                                                                                                                                                                                                                        SEQ ID NO 23119
LENGTH: 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23119, Application US/10437963 Publication No. US20040123343A1
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Best Local Similarity
                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(791)
OTHER INFORMATION: unsure at all n locations
FEATURE:
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                                                                                                                                    OTHER INFORMATION: Clone ID:
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 404
                            79 GCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTG
                                                                         Similarity
                                                                                                                                                                                                                           Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou, III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G 511
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Wu, Wei
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Pred. No. 4
                                                          Score 52.2; D
Pred. No. 5.2e
0; Mismatches
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RESULT 7
US-10-425-114-4414
; Sequence 4414, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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APPLICANT: Zhou, Yihua
APPLICANT: Screen, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tobaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 4414
LENGTH: N336
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 160; Conser
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                                                                                                          CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG
                                                                                                                                                                                 CACTTCATCGGCGGCACGCGCGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
                                                                                                                                                                                                                        GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG
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                                                                       TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG
                                                                                                                                              CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG
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Pred. No. 6.5e-05;
0; Mismatches 180;
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RESULT 8
US-10-425-114-29012
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; Sequence 17854, Application US/10425114
; Publication No. US20040034888A1
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LENGTH: 1394
TYPE: DNA
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                                                                                                                                                               GENERAL INFORMATION:
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Best Local Similarity 47.1%;
Matches 160; Conservative
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APPLICANT:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 73128
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FEATURE:
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Screen, Steven E
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Pred. No. 6.5e-05;
0; Mismatches 180; Indels
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; OTHER INFORMATION: Clone ID: LIB4828-011-H12_FLI
US-10-425-114-29011
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US-10-425-114-29011
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
SURGIH: 1598
TYDE: NNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17854
SEQ ID NO 17854
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29011, Application US/10425114 Publication No. US20040034888A1
                                                                          Matches 160;
                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                 ORGANISM: Zea mays
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                             679 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 ACTOTGOGOATTGACTACOGOTOCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
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ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 454
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ilarity 47.1%;
Conservative
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Pred. No. 6.6e-05;
0; Mismatches 180
                                                                                         Score 52;
Pred. No.
                                                                        Mismatches
                                                                                        DB 8; 1
                                                                        180;
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                                                                                                         Length 1598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: E.I. DuPont de Nemours & Company
APPLICANT: Yadav, Narendra
TITLE OF INVENTION: METHOD OF CONTROLLING SITE-SPECIFIC |
FILE REFERENCE: CL1975 US NA
CURRENT APPLICATION NUMBER: US/10/353,454
CURRENT FILING DATE: 2003-01-29
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Microsoft Office 97
SEQ ID NO 45
LENGTH: 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45, Application US/10353454
Publication No. US20030194809A1
GENERAL INFORMATION:
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Best Local
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                                                                          1099
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                                                                                                            TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                                                                                                                                                    CTCCGAGGGCGAGTCCATCTGGGÁGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1098
                                                                                                                                                                                        GTACAAGGACACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
                                                                                                                                                                                                                               GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCAACTCCAAGAAGATGCTGAAGGCCCTCCT 1038
                                                                                                                                                                                                                                                                                                         CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 978
                                                                                                                                                                                                                                                                                                                                                                                   CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCCTACTA 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG
CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1191
                                    CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA
                                                                          CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCCTCCTCGCCACCTTCATCAA 1158
                                                                                                                                                                                                                                                               GEAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51.4; DB 7;
Pred. No. 0.00011;
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                                      488
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PRIOR APPLICATION NUMBER: US/09/193,503B
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/09,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
UNMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4
LENGTH: 2346
                              US-10-353-445-5
; Sequence 5, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION: A NO. US20030119166A1el Method
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/10/353,445
CURRENT FILING DATE: 2003-01-29
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             APPLICANT: Baszczynski, Christopher L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
OTHER INFORMATION: sequence encoding a Cre:FLPm polypeptide, Cre
OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferrer
OTHER INFORMATION: codons) from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                               1518
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Rao, Guru
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                                                                                                                                                                                                                                                                                       CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
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                                                                                                                                                                                                                                         CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
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                                                                                                                                                                                                                                                                                                                                                                               CTCCGAGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457
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Gordon-Kamm, William J.
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Leszek
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Pred. No. 0.00011;
0; Mismatches 176;
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US-10-353-445-8

Sequence 8, Application US/10353445
Publication No. US20030119166A1
GENERAL INFORMATION:

APPLICANT: Baszczynski, Christopher APPLICANT: Lyznik, Leszek A. APPLICANT: Gordon-Kamm, William J.

APPLICANT: APPLICANT: APPLICANT:

Guan, Xuen Rao, Guru

Xueni

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1).
US-10-353-445-5
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APPLICANT: Guan, Suru
APPLICANT: Tagliani, Laura A.
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. US20030119166A1el Mei
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/10/353,445
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: US/99/193,503B
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR APPLICATION NUMBER: 60/096,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
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Best Local Similarity
Matches 157; Conserv
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OTHER INFORMATION: 6
OTHER INFORMATION: 6
OTHER INFORMATION: 6
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PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                             1578
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                                               CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA
                                                                                             CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637
                                                                                                                                          TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG
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CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA
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nilarity 47.1%;
Conservative
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Pred. No. 0.00011;
0; Mismatches 176;
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US-10-767-701-14768/c
Sequence 14768, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Koyalic, David K.
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; LOCATION: (1)...(2346)
US-10-353-445-8
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PRIOR FILING DATE: 1998-11-17
PRIOR PPLICATION NUMBER: 00/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR PPLICATION NUMBER: 60/65,613
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
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LENGTH: 2346
TYPE: DNA
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Best Local Similarity
Matches 157; Conserv
NUMBER OF
SEQ ID NO 1
                                           APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nuclecic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
PILE REFERENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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CURRENT FILING DATE: 2003-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre OTHER INFORMATION: from Bacteriophage Pl FEATURE:
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  F SEQ ID NOS: 63128
14768
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ilarity 47.1%;
Conservative
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Pred. No. 0.00011;
0; Mismatches 176;
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; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2086_1
US-10-767-701-14768
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Best Local Simi
Matches 125;
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                                                                                                             TGCGCGTCCCGCACAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCC 376
                                                                                      TGTACCGGCCCACGGCCCGCCGTCCTACACCGCCGACGGCTTCGAGATGAGCGTCG
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

8: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/AE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfiles1.seq:*
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T11 OCHECO 42, Application Uent No. 6114148 NERAL INFORMATION: APPLICANT: SEED, BRIAN APPLICANT: PARS, JURGE TITLE OF INVENTION: PR CORRESPONDENCE ADDRESS: STREET: 176 Federal CITY: BOSTON STATE: MA COUNTRY: USA ZIP: 02110 COMPUTER: ISM COMPAT COMPUTER: ISM COMPAT COMPUTER: ISM COMPAT COMPUTER: PASTSEQ FORM: MEDIUM TYPE: Diskett COMPUTER: OSE CURRENT APPLICATION DATA: APPLICATION NUMBER: FILLING DATE: 20-SEP- CLASSIFICATION NUMBER: FILLING DATE: APPLICATION NUMBER: FILLING DATE: APPLICATION NUMBER: FILLING DATE: APPLICATION NUMBER: FILLING DATE: APPLICATION NUMBER: ATTORNEY/AGENT INFORMAT NAME: EIBLING, KAZEN REGERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REFERENCE/DOC	,	44444444444444444444444444444444444444
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08717294 (LEVEL EXPRESSION OF EINS) ing LLP .reet Windows Version 2.0 Windows Version 2.0 Windows Version 2.0 100786/345001 TION: 42:	ALIGNMENTS	US-09-252-991A-15403 US-10-081-864A-23 US-10-081-864A-21 US-09-103-840A-2 US-09-103-840A-1 US-09-103-995-1 US-09-902-540-2667 US-09-902-540-1124 US-09-902-540-1127 US-09-902-540-484 US-09-902-540-484 US-09-902-540-484 US-08-804-198-1 US-10-632-694A-4 US-10-632-694A-4 US-10-632-694A-5 US-10-632-694A-5 US-10-632-694A-29 US-09-907-794A-249 US-09-907-795A-249 US-09-905-125A-249 US-09-906-700-249
		Sequence 15403, A Sequence 23, Appl Sequence 21, Appl Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1124, Ap Sequence 1124, Ap Sequence 1167, Ap Sequence 1167, Ap Sequence 1493, Ap Sequence 484, App Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 249, Appli

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ZIP: 2007-510>

COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TAMPUTER: IBM PC-DOS/MS-DOS
TAMPUTER: TOTAL PC-DOS/MS-DOS
TAMPUTER: TOTAL PC-DOS/MS-DOS
                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION UNMBER: 29,768
REFERENCE/DOCKET NUMBER: 1874
TELECOMMUNICATION INFORMATION:
TELEPHAN: 202 672 5399
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Krieger, T
TITLE OF INVENTION: S'
TITLE OF INVENTION: S'
TITLE OF INVENTION: PO
                                                                                 NAME/KEY:
LOCATION:
FEATURE:
FEATURE:
NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                    FEATURE:
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                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1993 CLASSIFICATION: 435
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                 TYPE: nucleic acid
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Jenish, David
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Butler, Michael J.
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STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES
POLYPEPTIDES
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GENERAL IN
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                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 23-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Krygsman, Phyllis
APPLICANT: Garven, Shelia
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                  NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 24-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W CITY: Washington, D.C.
                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328
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                                   202 672 5399
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Jenish, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malek, Lawrence T. Soostmeyer, Gisela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walczyk, Eva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Butler, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bartfeld, Daniel
SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Timothy
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                                                                                                                                                                     US 08/173,508
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                                                                                  18740/133/CACC
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Pred. No. 0.0027;
0; Mismatches 14
                                                                                                                                                                                                                                                                        Version
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FEATURE:

TOPOLOGY:

linear

NAME/KEY:

Sd

LOCATION:

104..1720

SEQUENCE CHARACTERISTICS:

1821 base pairs

TYPE: nucleic acid STRANDEDNESS: double

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RESULT 4
US-08-951-742-7
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US-08-265-310-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08951742 Patent No. 6127144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 136; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD FOR EXPRESSION OF PROTEINS TITLE OF INVENTION: BACTERIAL HOST CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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LOCATION:
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APPLICATION NUMBER:
                                                                                                                                   COUNTRY:
                                                                                                                                                                   CITY: Washington
                                                                                                                    ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087
                                                                                                                                                     D.C
                                                                                                                                      USA
                                                                                                                                                                                                                                                                                          Sheila Garven
                                                                                                                                                                                                                                                                                                          Eva Walczyk
Phyllis Krygsman
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ilarity 49.3%;
Conservative
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Lawrence T. Malek
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Michael J. Butler
                                                                                                                                                                                                                                                                                                                                                                                                                     Dany Hadary
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245..1720
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104..244
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US/08/951,742
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-951-742-7
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US-08-972-258-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1821 harr
                                                                       APPLICANT: Tagliani, Laura A.
APPLICANT: Zhao, Zuo-Yu
TITLE OF INVENTION: No. 5929301c
Patent No. 5929301
TITLE OF INVENTION: Recombinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.1%;
Best Local Similarity 49.3%;
Matches 136; Conservative
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Baszcz;
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ATTORNBY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                           CORRESPONDENCE ADDRESS:
                                                           NUMBER OF SEQUENCES:
                                                                                                                                                        APPLICANT:
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LOCATION:
STREET:
CITY: F
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
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Raleigh
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                                                                                                                                                                                                                                                                                   Application US/08972258
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             E: W. Murray Spruill 3605 Glenwood Ave.
                                                                                                                                                                                    Bowen, Benjamin A.
Drummond, Bruce J.
Gordon-Kamm, William J.
                                                                                                                                      Peterson, David J.
Sandahl, Gary A.
Tagliani, Laura A.
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104..1720
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245..1720
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                                                                                                          No. 5929301el Nucleic Acid Sequence Encoding
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                  Suite
                                                                            and
                                                                            Method of Using
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RESULT 6
US-09-263-128-1
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                                                                                                                                                                Sequence 1, Application US/09263128 Patent No. 6175058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
                                                                                                                                                GENERAL INFORMATION:
                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 27622
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: line MOLECULE TYPE: 1 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 919 420 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: US
COUNTRY: US
7TD: 27622
                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                 564
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                           GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGGCAGGAGTTCGTCGGCATGGTCTCGAG 215
                                                                                                                                                                                                                                                               CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596
                                                                                                                                                                                                                                                                                          CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
                                                                                                                                                                                                                                                                                                                                                            TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                                                                                                                                                                                                                                                                                                                                                                                             CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCTCCGAGGAGGCTGACAAGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCCAGCTGCGCGTCCCGCACCAGAG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA
   INVENTION:
               Bowen, Benjamin A.
Drummond, Bruce J.
Gordon-Kamm, William J
Peterson, David J.
Sandahi, Gary A.
Tagliani, Laura A.
Than Zuo-Yu
                                                                                                                             Baszczynski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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 No.
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                                                                                                                             Chris
 6175058el Nucleic Acid Sequence
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Pred. No. 0.0035;
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Encoding
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Recombinass
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: W. Murray Spruill
STREET: 3605 Glenwood Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2202
TELEFAX: 919 881 3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                             CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCCTCCTCGCCACCTTCATCAA
                                                                                           TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG
                                                                                                                                                          GTACAAGGACCACCATGAAGGAGGTCACCATGAAGGGCCCACGCCCACTCGGCAAACCT 395
                                                                                                                                                                                                                                                     CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA
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CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA
                                                                                                                        CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC
                                                                                                                                                                                       GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCCTCCT
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                             CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic sequence
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                                                                                                                                                                                                                                                                                                                                                                             Score 51.4; DB 3;
Pred. No. 0.0035;
0; Mismatches 176;
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596
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US-09-641-111A-1 RESULT 7

Sequence 1, Application US/09641111A Patent No. 6720475

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US-09-193-503B-4
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TITLE OF INVENTION: No. 6720475el Nucleic Acid Sequence Encoding
Patent No. 6720475
TITLE OF INVENTION: Recombinase and Method of Using Same
FILE REFERENCE: 35718/201942
CURRENT PAPLICATION NUMBER: US/09/641,111A
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/263,128
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 08/972,258
PRIOR FILING DATE: 1997-11-18
NUMBER: 0997-11-18
                                                                                                                                                               Sequence 4, Application US/09193503B Patent No. 6262341
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Best Local :
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APPLICANT: Baszczynski, Christopher L.
APPLICANT: Bowen, Benjamin A.
APPLICANT: Brummond, Bruce J.
APPLICANT: Gordon-Kamm, William J.
                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
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                              APPLICANT:
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FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1272)
OTHER INFORMATION: Optimized sequence
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Local Similarity 47.1%;
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F: Tagliani, Laura A.
INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
                                                                                                                                                                                                                                                                                                                                                             CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563
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                              Guan, A.
Guru
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                                                                                                    Baszczynski, Chri
Lyznik, Leszek A.
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                                                                                     Gordon-Kamm, William
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FITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/193,503B
CURRENT FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR APPLICATION NUMBER: 60/096,627
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR FILING DATE: 1997-11-18
SPIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver: 2.1
SOFTWARE: PatentIn Ver: 2.1
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Guan, Xueni
APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6262341el Method Fo:
TITLE OF INVENTION: A No. 6262341el Method Fo:
TITLE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/193,503B
CURRENT APPLICATION NUMBER: 60/099,435
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/065,613
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US-09-193-503B-5
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Best Local S
Matches 157
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Patent No. 6262341
GENERAL INFORMATION:
APPLICANT: Baszczynski, Christophe
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Nucleotide OTHER INFORMATION: Sequence encoding a Cre:FLPm polypeptide, Cre OTHER INFORMATION: from Bacteriophage Pl and FLP (Maize preferred OTHER INFORMATION: codons) from Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                 Baszczynski, Christopher
Lyznik, Leszek A.
Gordon-Kamm, William J.
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                                                                                                                                                                                                                                        For The Integration Of Foreign DNA
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RESULT 10
US-09-193-503B-8
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                                        SOFTWARE: Pat
SEQ ID NO 8
LENGTH: 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09193503B Patent No. 6262341
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SEQ ID NO 5
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                                                                                                           PRIOR APPLICATION NUMBER: 60/099,435
PRIOR TILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                     APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6262341el Method For The Integration Of Foreign DNA Into
TITLE OF INVENTION: Bukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/193,503B
CURRENT FILLING DATE: 1998-11-17
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: sequence OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage PI OTHER INFORMATION: FLP from Saccharomyces, both maize preferred OTHER INFORMATION: codons
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LOCATION: (1)..(2346)
ORGANISM: Artificial Sequence
                       TYPE: DNA
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Local Similarity 47.1%;
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                                                                                        PatentIn Ver. 2.1
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Gordon-Kamm, William J.
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                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/193,503
PRIOR FILING DATE: 1998-11-17
PRIOR PPLICATION NUMBER: 60/099,435
PRIOR APPLICATION NUMBER: 60/096,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR PILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 2346
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Lato
TITLE OF INVENTION: Eukaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
CURRENT FILING DATE: 1999-10-12
CURRENT FILING DATE: 1999-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baszczynski, Christopher
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ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description OTHER INFORMATION: sequence es OTHER INFORMATION: from Bacte:
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LOCATION: (1)..(2346)
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Gordon-Kamm, Wi
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Description of Artificial Sequence:Nucleotide sequence encoding a Cre:FLPm polypeptide, Cre from Bacteriophage P1 and FLP (Maize preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.4; DB Pred. No. 0.004; 0; Mismatches 1
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В
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TITLE OF INVENTION: Into
TITLE OF INVENTION: Enkaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
CURRENT FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US/09/193,503
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/096,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
PRIOR APPLICATION NUMBER: 60/065,613
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US-09-415-839-5
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                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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APPLICANT:
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                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 11
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                                                                OTHER INFORMATION: Description of Artificial Sequence: sequence OTHER INFORMATION: encoding mcCre:FLFm, Cre from Bacteriophage P1 and OTHER INFORMATION: FLP from Saccharomyces, both maize preferred OTHER INFORMATION: codons
NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                        ORGANISM: Artificial Sequence
                                              FEATURE:
                                                                                                                                                    FEATURE:
                                                                                                                                                                                              TYPE: DNA
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5. 6541231
  (1) .. (2346)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCAACTCCAAGAAGATGCTGAAGGCCCTCCT 1517
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Gordon-Kamm, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tagliani, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rao, Guru
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Pred. No. 0.004;
0; Mismatches 1
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APPLICANT: Guan, Xueni
APPLICANT: Rao, Guru
APPLICANT: Tagliani, Laura A.
TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
TITLE OF INVENTION: Into
TITLE OF INVENTION: Enkaryotic Genomes
FILE REFERENCE: 5718-66 (amended listing)
CURRENT APPLICATION NUMBER: US/09/415,839
CURRENT PILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 80/09/415,839
FRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/099,435
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/050,435
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: 60/050,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR APPLICATION NUMBER: 60/056,627
PRIOR FILING DATE: 1997-11-18
PRIOR APPLICATION NUMBER: 60/055,613
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
PRIOR FILING DATE: 1997-11-18
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Query Match
Best Local Similarity 47.:
Matches 157; Conservative
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                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE: FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Sequence OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from OTHER INFORMATION: Saccharomyces (maize preferred codons), and OTHER INFORMATION: from Bacteriophage P1
                                                                                                                   NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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o. 6541231
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Gordon-Kamm, Will
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Score 51.4; DB 3;
Pred. No. 0.004;
0; Mismatches 176;
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Pred. No. 0.004;
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                                            Length 2346;
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US-09-252-991A-13773/c
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PRIOR FILLING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 13773
LENGTH: 4131
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 13656
LENGTH: 8211
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PRIOR FILING DATE: 198-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABBUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Aav84068 Clone P5-
Aac61406 CNA enco
Acc129101 Rice abio
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Aad63718 pPH12891
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Adm99120 Bacterial	Abl11523 Drosophil	Adx09721 Plant ful	Ade10260 S. lavend	Aac55841 Complete	Ade10327 S. lavend	Aac55846 Mitomycin	Acl34434 Rice abio	Adx34980 Plant ful	Adx09781 Plant ful			Adx31428 Plant ful	-	Acl71569 M. xanthu	Abd14968 Pseudomon	Abd15052 Pseudomon	Abd15169 Pseudomon	Aad65094 Cre:FLPm	Aad65097 FLPm:Cre	Aad65095 Cre:FLPm	Acd26381 DNA encod	Acd26379 DNA encod	Acd26378 DNA encod	Aad10216 Chimeric	Aad10217 Chimeric	Aad10219 Chimeric

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ALIGNMENTS

RESULT 1 ADC16590

ADC16590;

18-DEC-2003

(first entry)

ADC16590 standard; DNA; 516

ВP

Scytalone dehydrogenase gene #SEQ ID 1.

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                                                                    Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.
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Example 2; SEQ ID NO 1; 50pp; Japanese.

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                                                                                                                                                                                                                                                                                                                                                                                                                       ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
ATCTTTGAGGACGGACGGAGACCTTTGGCGACAAA 516
                                                           GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG
                                                                                                   GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
                                                                                                                                                                                                                                                                                                                                          ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
                                                                                                                                                                                          ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGGAGGTACAAGGACACCACCATGAAGGAG
                                                                                                                                                                                                                      CTCCGCACGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrogenase gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%;
ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 A; 151 C; 156 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 514.4; DB 10;
Pred. No. 2.2e-107;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimizu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagayama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
them.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ase (SCDH),
optionally
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0

481

516

420 360 360 300 300

420

480

180 180 120 120 60

240 240

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RESULT 3
ADC16602
ID ADC1
XX ADC1
AC ADC1
XX Scyt
XX Magr
PN W02(
XX 18-6
XX Hagr
PN W2(
XX 18-6
XX WFI
XX (TSI
XX WFI
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XX Gen
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 515
                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
                                                                                                                                                                                                                                                                                                                                                                      Sequence 600 BP; 146 A; 176 C; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 3; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scytalone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC16602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaku K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002; 2002JP-00066955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2003; 2003WO-JP001980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC16602 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TSUB )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e encoding for scytalone dehydrogenase (SCDH), useful SCDH inhibitors and evaluating sensitivity to them.
                                                                                                                                                                                                       141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-748394/70
                                                                                                                                                  201
                                                                                                                                                                            121
               301
                                                                 241
                                                                                            261
                                                                                                                       181
                                                                                                                                                                                                                                                                                                                   515;
                                                                                                                                                                                                                                                                                                                                                                                                  in ADC16590.
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                                                                                                                                                 Watanabe S,
               ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                        CTCCGCACGCAGCACTTCATCGGCGGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTC
                                                                                             ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
                                                                                                                                                                                                                             ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
                                                                                                                                                                                                                                                           ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
                                                                                                                                                                                                                                                                                     ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
                                         CTCCGCACGCAGCATCATCGGCGGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTC
dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase DNA
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCDH; rice blast fungus; enzyme; inhibitor;
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В₽
                                                                                                                                                                                                                                                                                                                              Score 514.4;
Pred. No. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimizu T,
                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                      G; 110
                                                                                                                                                                                                                                                                                                                              .2e-107;
                                                                                                                                                                                                                                                                                                                                                                      T; 0 U;
                                                                                                                                                                                                                                                                                                                                            DB 10;
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ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG

ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG

140

60

120

200

닭

141

ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG

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RESULT 4
ADC16603
ID ADC1
XX ADC1
AC ADC1
XX Scyt
XX Scyt
XX Sext
XX Sext
XX Sext
XX Sext
XX Magin
XX 
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Query Match
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                                                                                                                                                          The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is given in ADC16592.
                                                                                                        Sequence 610 BP; 148 A; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scytalone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC16603 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAR-2002; 2002JP-00066955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 4; 50pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s encoding for scytalone dehydrogenase (SCDH), useful for screening SCDH inhibitors and evaluating sensitivity to them.
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                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KUMIAI CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
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                       99.7%;
99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawai K, Shimizu T,
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Score 514.4; | Pred. No. 2.3e. 0; Mismatches
                                                                                                        C; 170 G;
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                                                                                                           113 T; 0 U;
                          .3e-107;
                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagayama
                                                                                                              0 Other;
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                                                 Length
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                                                    610;
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RESULT 5
AAD54645
ID AAD5
XX AAD5
AC AAD5
AC AAD5
XX Stre
XX Poly
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XX Poly
XX Stre
FT CDS
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                                                                                                                                                                                                                                                                                                                                        antibiotic; amphotericin;
                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                             nodosus
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nodosus amphK
56829. .58019
/*tag= g
                                                                                                                                                                                                                                                                                    Location/Qualifiers complement(4. .1824)
                             /product= "Polyketide extension modules 18 a
                                                                               /product= "Polyketide
extension modules 15,
                                                                                                                                  /product= "Polyketide
extension modules 9, 1
                                                                                                                                                              amphDIII gene"
5042. .33574
                                                                                                                                                                                                                                               complement (1805. .3628)
                                                                                                              33584. .50518
                                                                                                                       nodosus amphI
                                                                                                                                                                                                                          /product= "ABC
                                                                                                                                                                                                                                                                  /product= "ABC transporter
                                                                                                                                                                                    /product= "GDP-mannose
                                                                                                                                                                                                       840. .4874
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16 and 17 encoded by
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S. nodosus
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                                                                                   Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, for preparing amphotericin derivative or analog antibiotic agent altered properties, in biosynthesis of polyketide other than
                                                                                                                      P-PSDB; AAE36116, AAE36117, AAE36118, AAE36119, AAE36120, AAE36121, AAE36122, AAE36123, AAE36124, AAE36125, AAE36126, AAE36127, AAE36128 AAE36129, AAE36130, AAE36131, AAE36132.
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                                                                                                                                                                                                                                                                           /*tag= q
/product= "Polyketide synthase multienzyme
extension modules 3, 4, 5, 6, 7 and 8 encod
nodosus by amphC gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (64324.
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complement(61798.
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complement(62051. .63250)
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nodosus amphDII gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (63250. .64308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product = "ORF3,
                                                                                                                                                                                                                                                                                                                                         'product= "Polyketide
                                                                                                                                                                                                                                                                                                                                                          product= "Polyketide synthase multienzyme housing loading module encoded by S. nodosus amphA gene" 0366. .79938
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98. .61995)
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The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polypene antibiotic amphotericin (amph) of Streptomyces nodosus. Polynucleotides of the invention are useful for preparing amphotericin derivatives or analogue antibiotic agents with altered properties and in the biosynthesis of polyketides other than amphotericin. amphDIII, amphDII or amphDII mutants are useful

Claim

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52-114;

276pp;

English

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Matches 159
               Wang
Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biosynthesis of perosaminyl-amphoteronolide B; amphDIII or amphDIII and amphN gene sequences are useful in the engineered biosynthesis of perosaminyl-16-descarboxyl-16-methyl amphoteronolide B; amphDIII, amphDIII and amphDI gene sequences are useful for preparing polypeptides capable of addition of mycosamine to a polyketide other than amphoteronolide A or B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine. The present sequence is S. nodosus amph biosynthetic gene cluster
                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene #23938
                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                              ACA42281 standard;
                                                                                                                                                                           21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                    WO200277183-A2
                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                         Antisense; ds; prokaryotic essential gene; cell proliferation;
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                                                          (ELIT-)
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               Zamudio C,
Trawick JD,
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Carr GJ,
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Pred. No. 0.031;
0; Mismatches 1
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             Haselbeck R, Yamamoto R,
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               Zyskind JW;
Xu HH;
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WPI; 2003-029926/02
P-PSDB; ABU38411.
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isolate candidate molecules for rational drug discovery programs. antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to

Claim 14; SEQ ID NO 30151; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued; (5) producing the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway of identifying a gene required for cellular proliferation or the test compound that inhibits gene product is or that has an activity against a biological pathway in which a proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the extent compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational conformation or screening for homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, conformation of promat directly from MIPO at the target of a compound that inhibits the conformation of the target of the printed specification, but was obtained in cells of the sequence is one of the target conformation of the compound that the sequence is one of the target conformation. The present sequence data for this patent did contonic format directly from MIPO at

Sequence 7407 BP; 1387 A; 2763 C; 2378 G; 879 T; 0 U; 0 Other;

Query Match Best Local Similarity

10.3%;

Score 53; Pred. No.

DB 8; œ --

Length 7407,

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G 7213
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                                                                                                                                                    AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT
                                                                                                                                                                                                            CAGAGGTACAAGGACACCACGATGAAGGAGGTCACCATGAAGGGCCACGCCACTCGGCA 390
                                                            AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGATTCGGGTAGCGTGCTGACCCTGACC
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Matches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                capable of altering the sensitivity of a microorganism to an antimicrobial agent by employing efflux pumps comprising polypeptides encoded by the following genes: PA1874, PA4142, PA2389, PA1876, PA4143, PA2390 or PA1163. The method is useful for identifying modulators of microbial resistance of an organism in a biofilm. The methods are also useful for identifying genes that encode proteins that play a role in biofilm resistance. The method is particularly useful for screening compounds or discovering compositions that will inhibit biofilm formation and overcome their resistance mechanisms. These methods are particularly useful in medical, industrial or natural settings, where formation of biofilms can have serious negative consequences and result in high costs both in human health and economic terms. The present sequence is a coding/control sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               efflux pumps containing polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7407 BP; 1387 A; 2763 C; 2378 G; 879 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 7; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying modulators of microbial resistance of organisms in biofilms, e.g. inhibitor of biofilm formation, by employing expression controls, c efflux pumps containing polypeptides, of genes associated with biofilm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biofilm; microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbial resistance gene PA1874 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DART-) DARTMOUTH COLLEGE
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                               6913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to a method of identifying a compound
                                                                                                       7033
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   451
                                                                                                     GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGGCGGGTTCGAC 7092
                                                                                                                                       CAGAGGTACAAGGACACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
                                                                                                                                                                        GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC
                                                                                                                                                                                                           CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC
                                                                                                                                                                                                                                             TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 6972
ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC
                                                                   AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                  Score 53;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                  DB 9;
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Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This synthetic gene codes for a human Factor-VIII protein that lacks the central B domain (amino acids 760-1639) of the native protein. In the synthetic gene, non-preferred or less preferred codons of the native gene (see AAV23339) are replaced by codons favored by highly expressed human genes to provide high-level expression in mammalian cells. The synthetic gene was assembled from 29 pairs of oligonucleotides (see AAV2340-97) which served as PCR templates. Synthetic genes of the invention (see also AAV23289-91) are used for production of recombinant proteins in mammalian cells at levels of at least 500% of those obtained using the natural genes. They can also be used in gene therapy. An expression vector comprising a synthetic gene and a mammalian cell harboring a synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New synthetic eukaryotic gene(s) - in which non-preferred or less preferred codon(s) are replaced to provide high level expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4451 BP; 972 A; 1568 C; 1234 G; 677 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Fig 13; 92pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic human Factor-VIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV23288 standard; DNA; 4451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mammalian cell(s).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7213 Ġ 7213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                   10.2%;
Similarity 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haas J;
                                                                                                                                                                                                                                                                                                      GCGACCCCACCCTCCGCACGCAGGAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCG
                                                      CCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGA
                                                                                                                                                                                     AGGACGAGGTCATCGGCTACCACCAGCTGCGCGCTCCCGCACCAGAGGTACAAGGACACCA
                                                                                                                                                                                                                                                             GCCACCCCAGCACGCGTCAGAAGCAGTTCAACGCCACCCCCCCGTGCTGAAGCGCCACC
CCATCAGCGTGGAGATGAAGAAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGA
                                                                                                                       AGCGCGAGATCACCCGCACCCTGCAAAGCGACCAGGAGGAGGATCGACTACGACGACA
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52.4; DB 2;
Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4451;
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RESULT 9
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                                    of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp seqdata uspto gov/sequence.html?DocID:2004034888. The polynucleotide
                             content. This polynucleotide
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 4414; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
(TABA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ield; plant growth; plant development;
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SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGATCGACGCCTCTGGAAGTTCGCCGGCCTCAA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DK,
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RESULT 10
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XX Plant
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Best Local
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yield; plant growth; plant development; seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADX54272 standard; cDNA; 1394
                                                                                             Liu J,
                                                                                                                                                                                                                                          (/noHZ)
(/rn17)
                                                                                                                                                                                                                                                                                                                05-NOV-2001; 2001US-00985678
                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
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                                                                                                                                                                                                                     (KOVA/)
                                                  2004-180133/17
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                                                                                                                                                                 KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                          LIU J.
                                                                                             Zhou Y,
                                                                                                                                            CAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTTCATCGGCGGCACGCCTGGGGAGAAGGTGTCCGAGGAGGACGAGGTCATCGGCTACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                            99US-00304517
                                                                                             Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
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                                                                                               Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>۾</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 1336;
                                                                                                  Tabaska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant growth regulator;
oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29012.
                                                                                               JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551
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New recombinant DNA construct, useful for improving plant tolerance

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RESULT 11
ADX35034
ID ADX35
XX ADX35
AC ADX35
XX 21-AP
DT 21-AP
CX Plant
XX Plant
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased resistance to plant disease, for producing galactomannan, Ilgnin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                     growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant g
                                                         plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding mark cold tolerance; heat tolerance; drought tolerance; herbicide t extreme osmotic condition; pathogen tolerance; pest tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring
                                                                                                                                                                                                             21-APR-2005
                                                                                                                                                                                                                                                      ADX35034;
                                                                                                                                                                                                                                                                                           ADX35034 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        improving
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                                                                                                                                                                     full length
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGTGATGGACTTCGTGAACAACGGGGGAGGTGTCCGGGGGTCACGCTGCTCAACTCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , drought, herbicides, extreme osmotic conditions, pathogens conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
  growth;
                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 349 A; 418 C; 365 G;
                                                                                                                                                                  insert polynucleotide segid 17854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29012; 15pp; English
                                                                                                                                                                                                                                                                                           cDNA; 1437
                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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plant growth regula oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1394
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                     growth regulator;
                                                                                                         marker;
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                                                                                   tolerance;
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                                                                                                                                                                                                                                                Matches 160;
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                       plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                Sequence 1437 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at the polynucleotide ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 17854; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathogousts, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-180133/17.
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(ZHOU/)
(KOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2003; 2003US-00425114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCRE/)
                                                                                                                                                                                                                                                                    Local
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TABASKA J E.
CAO Y.
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ZHOU Y.
KOVALIC D
                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                         CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG
                                                                                           CACTTCATCGGCGGCACGCGCGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC
                                                                                                                                                                                       ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA
                                                                                                                                                                                                                   TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG
                                                             CTGGTGATGGACTTCGTGAACAACGGGGGAGGTGTCCGGGGGTCACGCTGCTCAACTCCAAG
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2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                describes a recombinant DNA construct
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                                                                                                                                                                                                                                                                                                              364 A; 426 C; 375 G; 272 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                 Length 1437;
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GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC

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                        plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; recombinant DNA construct; physical array; plant breeding marker; recombinant construct; drought tolerance; heat tolerance; beat tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 29011; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-APR-2003; 2003US-00425114.
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       polynucleotide that can be used in the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001; 2001US-00985678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant DNA construct, useful for improving plant tolerance to d, heat, drought, herbicides, extreme osmotic conditions, pathogens ts, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-180133/17.
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ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou Y,
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Best Local Similarity
                                                             Bartfeld D,
Walcyzk E,
                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces lividans.
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    P-PSDB; AAR80506.
                       WPI; 1995-240673/31
                                                                                                                                                                                    23-DEC-1993;
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                                                                    Soostmeyer
                                                                                            Butler MJ,
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(first entry)
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245. . 1"
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Pred. No. 0.035
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                                                                                            Jenish DL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
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                                                                                            Krieger TJ,
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                                                                                            Malek LT;
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Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protease Tap-negative cells were transformed with a S. lividans 66 genomic library and screened with APA-beta-naphthylamide to isolate colonies contg. genes (AAQ99365-68) for novel proteases P5-4, P5-6, P5 and P8-2 (AAR80505-08). Impaired expression of such proteases by Streptomyces hosts improves the quality, quantity and stability of exogenous gene products. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endogenous Streptomyces protease(s), opt. having impaired activity useful in prodn. of exogenous proteins with reduced proteolytic degradation.
                                                                                                                                                                                                                                  Tripeptidyl aminopeptidase; TAP; N-terminal cleavage; GM-CSF; interleukin-3; IL-3; IL-6; EPO; tumour necros: IL-7; IL-2; P5-6; SlpD; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1821 BP; 283 A; 715 C; 602 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Fig 14; 142pp;
                            24-JUN-1994;
                                                   05-JAN-1999
                                                                          US5856166-A
                                                                                                            mat_peptide
                                                                                                                                    sig_peptide
                                                                                                                                                                                                              Streptomyces
                                                                                                                                                                                                                                                                                   Clone P5-6 encoding an aminopeptidase designated
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                                                                                                                                                                                                                                                                                                                                                              AAV84068 standard;
     23-DEC-1993;
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Pred. No.
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                                                                                                                                                                                                                                                 inal cleavage; protein production;
tumour necrosis factor; TNF; SCF;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces tri:peptidyl aminopeptidase pro-peptide from secreted proteins.
                                                                                                                                                                                                                                                       Subtilisin-like polypeptide; protein production; GM-CSF; chloromethylketone aminopeptidase inhibitor; stem cell factor; granulocyte macrophage-colony stimulating factor; interleukin-3; IL-6; erythropoietin; EPO; SCF; IL-7; IL-2; ds.
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Soostmeyer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC61406 standard; cDNA; 1821
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                          sig_peptide
                                                                                                                                                                                                 Streptomyces
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Similarity 49.3%;
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W, Krygsman
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Pred. No. 0.036;
0; Mismatches 14
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P, Kriege
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Krieger TJ;
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Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a subtilisin-like polypeptide (Ssp). The polypeptide is a protease, and was used to identify inhibitors, which were then used in the method of the invention. The specification describes a method for producing a heterologous protein. The method involves incubating a Streptomyces host cell transformed nucleic acid sequence encoding the heterologous protein, in the presence of a peptide-substituted chloromethylketone aminopeptidase inhibitor. The inhibitor has the structure X-proline-Y-chiromethylketone, where X is an aliphatic or hydroxy amino acid and Y is an aliphatic hydroxy or sulphur-containing amino acid. Alternately, X and Y are non-polar amino acids. Use of the inhibitor inhibits degradation of the heterologous protein by aminopeptidases. The method is useful for producing granulocyte macrophage-colony stimulating factor (GM-CSF), interleukin-3 (IL-3), IL-6, erythropoietin (EPD), stem cell factor (SCF), IL-7, and IL-2 which are
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P-PSDB;
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GACGACCTGGACGCGAAGCCCCTGCCCGGCGGCGAC 1123
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S, Walczyk E,
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Scoring table: Sequence: IDENTITY_NUC Gapon 10.0 , Gapext 1.0 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa

Searched: Total number of hits satisfying chosen parameters: 6366136 seqs, 31973710525 residues

12732272

Minimum Maximum DB Bd seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Listing first 45 summaries Maximum Match 100%

Database : 10: 11: 12: 13: 14: 15: GenEmbl: * gb_sts:
gb_sy::*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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162.4	167.8	171.8	179.2	179.2	179.2	182.4	182.6	185.6	187.8	189.4	190	191.8	192	219	234.8	251.2	514.4	Score
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10.0	10.0	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.3	10.3	10.3	10.3	10.3	10.3	10.4	10.5	10.7	11.4	30.2	31.0
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ALIGNMENTS

JOURNAL PUBMED REFERENCE AUTHORS REFERENCE AUTHORS TITLE RESULT 1
ABOU4741
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM FEATURES COMMENT TITLE JOURNAL gene CDS source Direct Submission
Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Miclobial Toxicology Lab.;
2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan
(B-mail:tmotoyam@postman.riken.go.jp, Tel:+81-48-467-9518)
Sequence updated (27-Oct.1998). Motoyama, T., Imanishi, K. and Yamaguchi, I. cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pathogenicity of the rice blast fungus, Pyricularia AB004741.1 GI:3798733 scytalone dehydratase; sdhl. Magnaporthe grisea Magnaporthe grisea Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998) 9571787 Magnaporthe grisea mRNA AB004741 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. Motoyama,T. AB004741 (bases 1 to 807) (sites) /gene="Sdh1" 81. .599 /organism="Magnaporthe grisea"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:148305"
/note="sequence obtained from anamorph Pyricularia oryzae
whose telemorphic form is unknown" /gene="Sdh1" /codon_start=1 /product="scytalone_dehydratase" /protein_id="BAB34046.1" /db_xref="GI:3798734" ocation/Qualifiers .807 .807 807 bp mRNA linear PLN 13-NOV-1998 for scytalone dehydratase, complete cds.

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Tel:81-852-32-6520, Fax:81-852-32-6597)

(ibases 1 to 770)

Rihara, J. and Moriwaki, A.

Rihara, Shimane University, Faculty of Life and Environmental Science; Nishikawatsu 1060, Matsue, Shimane 690-8504, Japan (E-mail:j-khiara@life.shimane-u.ac.jp, Tel:81-852-32-6520, Fax:81-852-32-6597)
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                                                                                                                                          Kihara, J., Moriwaki, A., Ueno, M., Tokunaga, T., Arase, S. and Cloning, functional analysis and expression of a scytalone dehydratase gene (SCD1) involved in melanin biosynthesis of phytopathogenic fungus Bipolaris oryzae
Carr. Genet. 45 (4), 197-204 (2004)
                                                                                                                                                                                                                                  Bipolaris oryzae
Bipolaris oryzae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
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TLRIDYRSFLDKLWEAMPAEEFVGMVSSKQVLGDFTLRTQHFIGGTRWEKVSEDEVIG
YHQLAVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDR
IFEDGRETFGDK"
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D86079.1
                                                                      melanin biosynthesis; scytalone
Colletotrichum lagenarium
Colletotrichum lagenarium
Eukaryota; Fungi; Ascomycota; Posordariomycetes incertae sedis;
Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Cloning and structural analysis of the GCD1 encoding scytalone dehydratase in G
                                                                                                                                                                                             COGSCD1 11
Colletotrichum lagenarium
                                                           mitosporic Phyllachoraceae;
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nilarity 70.8%;
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KIDYRSFLDKIWEAMPADEFVAMASDPAVLGNPLLKTQHFIGGTRWEKTAEDEITGYH
QLRVPHQRYTDESRATVAVKGHAHSFNTHWYKKIDGEWKFAGLNPDIRWYEYDFDKVF
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/codon_start=1
/product="scytalone_dehydratase"
/protein_id="BAC79365.1"
/db_xref="GI-32879677"
/db_xref="GI-32879677"
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strain="D9/F6-69"
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Pred. No. 3.1e-52;
0; Mismatches 138
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um DNA for
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, Tajima,S. and Furusawa,I. melanin biosynthesis gene Colletotrichum lagenarium
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s; Phyllachoraceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant Pathology, Faculty of Agriculture, Kyoto Prefectural University; Shimogamo, Kyoto Kyoto 606, Japan (B-mail:y_kubo@kpu.ac.jp, Tel:075-702-0957, Fax:075-702-0957)
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 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC
                                 GTGCCGCACCAAAAGTACACCGACGCCTCGCGCACCGAGGTCGCCGTCAAGGGCCACGCC
                                                             GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC
                                                                                              GCCATGATCTCGGACAAGTCCGTCCTCGGCAACCCCGCTCCTCAAGACGCAGCACTTCATC
                                                                                                                                                                                                                         ATCGACTACCGCTCCTTCCTCGACAAGATCTGGGGAGGCCATGCCCGCCGAGGAGTTCATC
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join(233.
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267. .323
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Idyrsfldkiweampaeefiamisdksvlgnpllktohfiggsrwekvsdtevighho
lrvphokytdasktevavkchahsynmhwyrkvngvwkfaglmeeirwsbydfdavfa
dgrdsygtedoktdvkvvekeikfaaah"
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/product="scytalone dehydratase"
/protein id="BAA13009.1"
/db_xref="GI:1395160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              122. .488
/gene="SCD1"
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                                                                                                                                                                     276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ophiostoma floccosum
Ophiostoma floccosum
Ophiostoma floccosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostom
1 (bases 1 to 1477)
Wang, H.L., Kim, S.H. and Breuil, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang,H. and Breuil,C.
Direct Submission
Submitted (25-OCT-2000) Wood Science,
Columbia, 2424 Main Mall, Vancouver, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A scytalone dehydratase gene from Ophiostoma floccosum restores the melanization and pathogenicity phenotypes of a melanin-deficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete cds.
AF316575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF316575 1477 bp DNA linear PLN 22-MAY-2002
Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF316575.1 GI:12964737
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                                                                                                                            ACCTITGGCGACAA 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAGCTACAACATGCACTGGTACCGCAAGGTCAACGGCGTGTGGAAGTTCGCCGGTCTG
              GGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTC
                                                                            TCGTACGGCACCGA 862
                                               (bases 1 to 1477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genet. Genomics 266 (1), 126-132 (2001)
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                              /product="scytalone dehydratase"
/protein id="AAK11296.1"
/db.xref="G1:12946738"
/translation="MGINISSITSTTSSAPKTTGSDISFEDYMGLCSAAYEWADSYDS
KDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDFSVLGNPLLRTQHFFGAS
                                                                                                                                                                                                                                                 RWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKFAGLD
PKIRWFEYDFDKVFASGRDQFGTEEKAAATAGPELLAKDKVQSAIASAQRAVAVSA"
                                                                                                                                                                                                                                                                                                                                                                                                                     join(<316. .394,471. .571,635. .>1105)
/gene="OSD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Ophiostoma
/mol type="genomic DNJ
                                                                                                                                                                                                                                                                                                                                                                           'gene="OSD1"
                                                                                                                                                                                                                                                                                                                                                                                        /product="scytalone dehydratase"
join(316._.394,471. .571,635. .1105)
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                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:104300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="387N"
                                                                                                                                                                                  42.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   پرستاostoma floccosum"
_type="genomic DNA"
in="387N"
                                                                                                                                                                     0;
                                                                                                                                                                                  Score 219; DB 4
Pred. No. 4e-44;
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                                                                                                                                                                       Mismatches
4.
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                                                                                                                                                                       95;
                                                                                                                                                                                                  Length 1477;
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AY098662
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                                                                                                           Query Match
Best Local Similarity
Matches 231; Conserv
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                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 bp DNA linear PLN 16-JAN-2
Ophiostoma piliferum isolate Cartapip scytalone dehydratase (SD)
gene, partial cds.
AY098662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-APR-2002) Wood Science, Columbia, 4th Floor, 2424 Main Mall, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ophiostoma piliferum
Ophiostoma piliferum
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fleet,C. and Breuil,C.
Inhibitors and genetic analysis of scytalone dehydratase
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 16(11), 1331-1339 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY098662.1
                                                                   TCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGGCGACAA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAAGATCCGCTGGTTCGAATACGATTTTGATAAGGTGTTTTGCCAGCGGCCGCGACCAG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGGCCAACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCCGGCCTCGAT 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCAC
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          rect Submission
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(bases 1 to 415)
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Breuil, C.
                                                                                                                                                                                              /gene="SD"
/codon_start=1
/codon_start=1
/product="scytalone_dehydratase"
/protein_id="AAM34808.1"
/db_xref="GI:21238834"
/translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
/translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                                                                                                                                                                                            AHSANTHWYRKVDGVWKFAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Ophiostoma piliferum"
/mol_type="genomic_DNA"
/isolate="Cartapip"
                                                                                                                                                                                                                                                                                                                          /product="scytalone dehydratase"
join(<1. .69,120. .>415)
                                                                                                                                                                                                                                                                                                                                                           join(<1. .69,120.
/gene="SD"
                                                                                                                                                                                                                                                                                                                                                                                          gene="SD"
                                                                                                                                                                                                                                                                                                                                                                                                                             country="USA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="taxon:38032"
                                                                                                                         37.2%;
78.0%;
                                                                                                           0
                                                                                                         Score 192; DB 4;
Pred. No. 2.2e-37;
0; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , University of British Vancouver, BC V6T1Z4, Canada
                                                                                                           65;
                                                                                                                                        Length 415;
                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY214004 1215 bp DNA linear PLN 10-
Ceratocystis resinifera syctalone dehydratase I (SDI) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-JAN-2003) Wood Science, University of British Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Microascales; Microascales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               resinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTCGGCCAACACCCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1215)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cds.
                                                       545. .934
/gene="SD1"
                                                                                                                         /number=1
379. .476
                                                                                                                                                                                                          /translation="mvAGSSDSTQVTASTVNPKTISFEDYCGLNTALYEWADSYDSKD
WDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQHFVGASRW
ERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKFAGLYPE
                                                                                        /gene="SD1"
/number=2
                                                                                                                                                                                                                                                       /product="syctalone dehydratase
/protein_id="AAO60167.1"
/db_xref="GI:37787190"
                                                                                                                                                                                                                                                                                                                                                                         joın(<233. .305,379. .476,545. .>934)
/gene="SD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                        "gene="SD1
                                                                                                                                                                                                                                                                                                                                        product="syctalone dehydratase I"
oin(233. .305,379. .476,545. .934)
                                                                                                                                                                                                                                                                                                                                                                                                            'gene="SD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                           'country="Canada: Alberta, Edson"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Ceratocystis
/mol_type="genomic DNA"
/isolate="EL3-21"
                                                                                                                                                                                          RWSEYDFDKVFASGREEFGDEDIDV"
                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                            gene="SD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ecific_host="Pinus contorta"
_xref="taxon:95837"
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Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 414)
Fleet, C. and Breuil, C.
Direct Submission
Submitted (22-APR-2002) Wood Science, University of British Submitted (22-APR-2002) Wood Science, University of British
Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V671Z4, Canada
                                                                                                                                                                                                                                                                                                                                                                                              Ophiostoma piliferum
Ophiostoma piliferum
Ophiostoma piliferum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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AY098664
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/db_xref="GI:21238838"
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/product="scytalone dehydratase"
join(<1. .69,120. .>414)
                                                                                                                                                        /organism="Ophiostoma piliferum"

/mol type="genomic DNA"

/isolate="201-1A"

/db xref="taxon:38032"

/country="Austria"
                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                               'gene="SD"
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AHSANTHWYRKVDGVWKFA"
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	CDS	mRNA	gene		FEATURES source	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	AUTHORS TITLE	-	SOURCE	Z	AY098663 LOCUS DEFINITION	2 E	_	D 42		·ω	იხ 2	0у 2	Db 1	Qy 1	Db 1	Qy 1	Query Match Best Local Matches 23
/codon_start=1 /product="scytalone dehydratase" /protein_id="AAM34809.1"	/gene="SD" /gene="SD"	/gene="SD" join(c1 .69,119>414) /gene="SD"	/country="United Kingdom" <1414 /carae="RSD"	/organism="Ophiostoma piliferum" /mol type="genomic DNA" /isolate="198-20E" /db_xref="taxon:38032"	Location/Qualifiers 1. 414	Direct Submission Submitted (22-APR-2002) Wood Science, University of British Columbia 4th Floor 2024 Main Mall Vancouver BC VKT174 Canada	es. 106 (11), 1331-1339 (2002) s 1 to 414) and Breuil,C.	Fleet, C. and Breuil C. Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi	Ophiroscome priliferm Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma. 1 (hasea 1 to AlA)	Ophiostoma piliferum	ĀY098663 ĀY098663.1 GI:21238835	AY098663 AY098665 AY09665 AY09665 AY098665 AY098665 AY098665 AY098665 AY098665 AY098	05 PAGELLOCCE	7	45 GTCAAGGGCCACTCGGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGG	η υ α	07 TACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACC	25 ACCCAGCACTTCTTCGGCCCTCGCGCTGGGAGGCGCATCTCCGACACCGAGGTCGTCGGC 284	247 ACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGC 306	165 GCCGACGAGTTCATCGGCATGATCTCCGACCCCAGCGTGCTCGGCAACCCGCTGCTGCGC 224	187 GCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGC 246	105 GCTGCTGACCGACAGATCGACTACCGCTCGTTCCTCAACAAGCTGTGGGAGGCCATGCCG 164	127 GCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCG 186	ch 36.8%; Score 190; DB 4; Length 414; il Similarity 75.8%; Pred. No. 7e-37; 235; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

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Ophiostoma minus
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                          Submitted (22-APR-2002) Wood Science, Columbia, 4th Floor, 2424 Main Mall, Location/Qualifiers
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Ophiostoma minus isolate
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                                                                                                                                                       /mol
                                                                           join(<1.
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                                                                                                    country="Canada"
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75.6%;
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Pred. No. 1e-36;
0; Mismatches
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58-4 scytalone dehydratase
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BC V6T1Z4, Canada
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Ophiostoma piceae
Ophiostoma piceae
Ophiostoma piceae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Enrdariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiosto
                                                                                                                                                                                                                                                 Direct Submission
Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4,
                                                                                                                                                                                                                                                                                                                         Fleet,C. and Breuil,C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11),
2 (bases 1 to 427)
Fleet,C. and Breuil,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ophiostoma piceae isolate partial cds. AY098656
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MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
AHSANQHWYRKVDGVWKFAG"
             /yene="SD"
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/db_xref="GI:21238826"
product="scytalone dehydratase"
                                                                                                            'country="Canada"
                                                                                                                                                                                                  organism="Ophiostoma"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                       'isolate="AU1"
                                                                                                                                                                         mol_type="genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:21238821
                                                                                                                                  xref="taxon:61273"
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Pred. No. 2.5e-36;
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join(<1. .69,132./gene="SD"

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ORIGIN

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ACCESSION
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KEYWORDS
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REFERENCE
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AY098657
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                                                                                                                                                                                                                                                                                                                         Inhibitors and genetic analysis of scytalone dehydratase the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)

2 (bases 1 to 424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ophiostoma floccosum partial cds.
                                                                                                                                                                                                                                                                Submitted (22-APR-2002) Wood Science, Columbia, 4th Floor, 2424 Main Mall, V
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ophiostoma floccosum
Ophiostoma floccosum
                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                     Fleet, C. and Breuil, C.
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Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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                                                                                                                                                                                                                                                                                                           and Breuil, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="Ewadrydskdwdrlrkciaptlridyrsflnklweampaeefig
MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH
AHSANTHWYRKVDGVWKFAG"
                                                                                                                   /gene="SD"
join(<1. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="scytalone dehydratase"
/protein_id="AAM34802.1"
/db_xref="GI:21238822"
/codon_start=1
/product="scytalone dehydratase"
/prottein_id="AAM34803.1"
/db_xref="GI:21238824"
                                                                                                                                                                                                          /mol
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                         /product="scytalone
join(<1. .69,132. .:
                                                                                                     gene="SD"
                                                                                                                                                                                              /isolate="GR10"
                                                                                                                                                                                                                     organism="Ophiostoma floccosum"
                                                          gene="SD"
                                                                                                                                                            country="United Kingdom"
                                                                                                                                                                           db_xref="taxon:104300"
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76.7%;
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                                                                                                                                                                                                                                                                               University of British
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AY098659
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Ophiostoma minus isolate OM3
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                                                                                                                                                                                                                                                                                                                                                                                           Ophiostoma minus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCCACGCAGCACTTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCC
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AHSANTHWYRKVDGVWKFA"
/translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
MISDPSVLGNPLLRTQHSFGASRWGRVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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/protein_id="AAM34805.1"
/db_xref="GI:21238828"
                                                                                                            /product="scytalone dehydratase"
join(<1._69,133. .>428)
                                                                                                                                               gene="SD"
                                                                                                                                                                                                                                               /organism="Ophiostoma minus"
/mol_type="genomic DNA"
/isolate="OM3"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                             gene="SD"
                                                                                                                                                                               'gene="SD"
                                                                                                                                                                                                                country="United Kingdom"
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les 69;
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DEFINITION

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Best Local Similarity
Matches 225; Conser
 Query Match
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                                                                                                                                                                       CDS
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AY098661
                                                                                                                                                                                                                                                                                                                                                                                                                               Fleet,C. and Breuil,C. Inhibitors and genetic analysis of scytalone dehydratase the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)

2 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ophiostoma piceae
Ophiostoma piceae
                                                                                                                                                                                                                                                                                                                                                                    Submitted (22-APR-2002) Wood Science, University Columbia, 4th Floor, 2424 Main Mall, Vancouver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ophiostoma piceae

Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Ophiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY098661.1
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                                                                                                                                                                                                                                                                                                                                                                                                                    Fleet,C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTGGCCGTCAAGGGCCACGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                  and Breuil, C.
                                            /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
AHSANQHWYRKVDGVWKFAG"
                                                                                                                                                                                        /gene="SD"
                                                                                                                                                                                                                                              /country="Austria"
<1. .>421
                                                                                                                                                                                                                                                                                        /organism="Ophiostoma piceae"
/mol type="genomic DNA"
/isolate="W5"
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                         /Codon_start=1
/product="scytalone dehydratase"
/protein_id="AAM34807.1"
/db_xref="GI:21238832"
                                                                                                                                                   gene="SD"/
                                                                                                                                                                   join(<1. .69,126. .>421)
                                                                                                                                                                                                                                /gene="SD"
                                                                                                                                                                                  product="scytalone dehydratase"
                                                                                                                                                                                                                                                                            db_xref="taxon:61273"
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76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ophiostoma piceae
Ophiostoma piceae
Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordaric
Eukaryota; Fungi; Ascomycota; Ophiostomataceae;
                                                                                                                                                                                                                                                                                                                                                                           Fleet,C. and Breuil,C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DMN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 423)
                                                                                                                                                                                                                                                                                                                  Submitted (22-APR-2002) Wood Science, Columbia, 4th Floor, 2424 Main Mall,
                                                                                                                                                                                                                                                                                                                                               Fleet, C. and Breuil, C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY098660.1
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AY098660
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/translation="ewadrydskdwdrlrkciaptlridyrsflnklweampadefig
misdpnvlgnpllrtqhffgasrwervsdtevigyhqlrvphqvytdaslstvavkgh
ahsanqhwyrkvdgvwkfag"
                                                                                                                                             /yezn(<1. .69,128. .>423)
/gene="SD"
                                                                                                                                                                                                                                                                                     1. .423
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/protein_id="AAM34806.1"
/db_xref="GI:21238830"
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join(<1. .69,128. .>423)
                                                                                                                                                                                                             /country="Canada"
                                                                                                                                                                                                                           /mol_type="genomic_DNA
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ataceae; Ophiostoma.
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Query Match Best Local Similarity Matches 223; Conserv

Conservative

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75.3%;

Score 179.2; DB 4 Pred. No. 3.7e-34; 0; Mismatches 73

DB 4;

Length

423;

Indels

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Gaps

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Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 423)
Fleet, C. and Breuil, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY098666 423 bp DNA linear PLN 16-JAN Ophiostoma setosum isolate NZFS3734 scytalone dehydratase (SD)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma
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ALIGNMENTS

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; ORGANISM: Acinetobacter baumannii US-09-328-352-4170
APPLICANT: GARY BRETON

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
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APPLICANT: GATY L. BIRCTON et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                             Sequence 4649, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4170
LENGTH: 153
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                              135 Y--KKIDGVWKFAGL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 MLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 DYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQ
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                                                                                                                          AMINO ACID SEQUENCES RELATING THERAPEUTICS
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RESULT 4
US-09-625-634A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-625-634A-3
                               GENERAL INFORMATION:
APPLICANT: Vernet, Corine
APPLICANT: Rastelli, Luca
APPLICANT: Herrmann, John
TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                         Sequence 2, Application US/09625634A Patent No. 6653448
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Vernet, Corine
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Herrmann, John
TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: USSN 60/194,256
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: USSN 60/192,838
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Cura-244 (15966-744) US
CURRENT APPLICATION NUMBER: US/09/625,634A
CURRENT FILING DATE: 2000-07-26
FILE REFERENCE: Cura-244 (15966-744) US CURRENT APPLICATION NUMBER: US/09/625,634A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus sp.
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ORGANISM: Proteus mirabilis
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                                                                                                                                                                                                                                                                                                                                                                                                                              y match
Local Similarity 31.1%; Pred. No. 0.4;
hes 32; Conservative 11; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                              74
                                                                                                                                                                                                                                                                                                                                                                                                 84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 KVSEDEVIGYHQLR------VPHQRYKDTTMKEVTMKGHAHSANLHWYKK--IDGVW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 WDKAQR-----EDVLDKMFETAP-QSFV-----WLADLCLRGAKHTLQRTSWE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 WDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLR-TQHFIGGTRWE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKARYHFGGRLHSREAGIKPFISTVRQGFWGYY 223
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                                                                                                                                                                                                                                                                               CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                                                                                                                                                                                                                                                                                                            QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
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;; Pred. No. 0.38
18; Mismatches
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                                                          AND NUCLEIC
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                                                            ENCODING
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; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-29072
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-625-634A-2
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US-09-248-796A-15811
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US-09-252-991A-29072
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; Patent No. 6747137
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
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PRIOR APPLICATION NUMBER: USN 60/194,256
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: USSN 60/192,838
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.1:
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LENGTH: 700
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29077
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                          112
                                                                                                                                                                                                                                                                                                                                                                                                                        141 EDQPAEQRLGQRVAPGHILGYPEDRVAHRVQRSPQCRQAVAEVVEQGEDVGHHHIEEGHQ 200
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                                                                                                                                                                                                                                                                                                                                                                          RYK----DTTMKEVTMKGH--AHSANLH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAMPAEEFVGM-VSSKQMLGDPTLRTQHFIGGTRW-----EKVSEDEVIGYHQLRVPHQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137
                                                                                                                                                                                                                                                                                                                               RHRRQQEGDSALLEAVPDAHESIHRSVLH 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%; Score 77; DB 28.1%; Pred. No. 6.6;
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RESULT 8
US-09-489-039A-11131
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Sequence 11131, Application US/09489039A Patent No. 6610836
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Tocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PA
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 5288
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SEQ ID NO 15811
LENGTH: 602
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APPLICANT: Nano, F
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PRIOR FILING DATE: 1996-06-14
PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1995-06-15
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 0899 PRIOR FILING DATE: 1997-12-15
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CURRENT FILING DATE: 2000-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 437
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                                                                                                         158 FYYNK--AAWQQAGL-PDRGPQSWSEFDEWGPELQRVVGAGRSAHG
                                                                                                                                           133 HWYKKIDGVWKFAGLKPD---IRWGEFD----FDRIFEDGRETFG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 FLPQERVAEFAGLSPEKLLMETERTLGDGHLLIMHEDLIAKDNESQQLGNKIKDIEGRLA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103
                                                                                                                                                                            100 LLDDRWWFHFALSGVLTALDDLFG--QVGVDTTDYVDSLLADYEFNGRHYAVPYARSTPL
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                                                                                                                                                                                                                                                    43 WSSHPGQ---SSAAERELIGRFQDRFPTLSVKLIDAGKDYDEVAQKFNAALIGTDVPDVV
                                                                                                                                                                                                                                                                                      58 WEAMPAEEFVGMVSSKQMLGD-----PTLRTQHFIGGTRWEKVSE-------
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Similarity 21.3%;
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20.5%; Pred
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Pred. No. 6.7;
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Pred. No.
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PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11131
LENGTH: 768
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                      INFORMATION FOR SEQ
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                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 10
SEQUENCE CHARACTERISTICS:
                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 29-JUI
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STREET: 1
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                                                         TELEPHONE:
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1100 New York Ave.,
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Beaulieu, Car
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                                      202-371-2540
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20.6%; Pred. No.
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US-09-328-352-7847
US-09-328-352-7847
; Sequence 7847, Application US/09328352
; Patent No. 6566958
; GANERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8407
LENGTH: 518
TYPE: DET
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US-09-489-039A-8407
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GENERAL INFORMATION:
APPLICANT: GARY Breton et. al
APPLICANT: GARY BRETON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DEFERENCE: 2709.2004001
TITLE DEFERENCE: 2709.2004001
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Matches
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Best Local Similarity 21.9
Matches 33; Conservative
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TOPOLOGY: bol
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Local Similarity 26.1%; Pred. No. 14;
Les 36; Conservative 16; Mismatches
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21.9%; Pred. No. 9
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RESULT 12
US-09-949-016-11697
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                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11697
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Best Local S
Matches 35
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows
SEQ ID NO 11697
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                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 IGGPGRKRSAVKVWEQRKYQNLDDDQVLGTRQMQIALRRLRKFARQGAAEELDVDGTIRE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 -- LQKAGSLEELMKWLEER-----LREQHKKHQGGNRMVGTGGTSPFGAFGDHPEGVR 157
146
                                    139
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                                                                       98 WRLR--HFVGWVWYER----EVI-----LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 145
                                                                                                            79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
                                                                                                                                                                                    29 SYDSKDWDRLRKVIAPTLRIDY----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 7.6%; Score 72; DB 1 Similarity 18.9%; Pred. No. 11; 35; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 DEITFSDYLGLMTCVYEWADSYD-----SKDW---DRLRKVIAPTLRIDYRSFL
                                   DGVWKFAGLKP 149
                                                                                                                                                 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD
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 DTLEHEGGYLP 156
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                       7.6%; Score 71.5;
26.0%; Pred. No. 18;
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RESULT 13 US-09-149-727-5

Sequence 5, Application US/09149727 Patent No. 6391547

GENERAL INFORMATION

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SEQ ID NO 5
LENGTH: 613
TYPE: PRT
ORGANISM: Homo sapiens
US-09-149-727-5
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US-09-270-957-16
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APPLICANT: Richard A. Jefferson and Jorge E. Mayer
TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES,
TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
FILE REFERENCE: 190106.405C1
CURRENT APPLICATION NUMBER: US/09/270,957
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
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Patent No. 6641996
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Best Local :
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CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: US 60/058,263
EARLIER FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jefferson, Richard A.
APPLICANT: Kilian, Andrzej
APPLICANT: Keise, Paul Konrad
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 190106.405
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 613
TYPE: PRT
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                                                                                                                         79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
                                                                                                                                                                      15 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD
                                                                                                                                                                                                                 29 SYDSKDWDRLRKVIAPTLRIDY-----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 WRLR--HFVGWVWYER----EVI-----LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD
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DTLEHEGGYLP 128
                                      DGVWKFAGLKP 149
                                                                                   WRLR--HFVGWVWYER---
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                                                                                   --LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 117
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RESULT 15 US-09-715-858-2

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Search completed: December
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; SEQ ID NO 2
; LENGTH: 651
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APPLICANT: Podsako
APPLICANT: Watson,
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                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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APPLICANT: Couto, Linda B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
TITLE OF INVENTION: TREATMENT OF LYSOSOMAL DISORDERS
EITE DEFENCE. OF ONO ACC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/715,858
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 16
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                                                         138 DTLEHEGGYLP 148
                                                                                                  139 DGVWKFAGLKP 149
                                                                                                                                           90 WRLR--HFVGWVWYER----EVI-----LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 137
                                                                                                                                                                                 79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
                                                                                                                                                                                                                            35 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD
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26.0%; Pred. No. 25;
ative 19; Mismatches
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  2006, 01:29:07
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Database
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                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
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                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
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1: geneseqp198
2: geneseqp199
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942
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	IJ	4	ω	2	<u>, , , , , , , , , , , , , , , , , , , </u>	Result
18	81	81	81	81	81	81	81	18	83	84	84	84	84	84	84	85	86.5	86.5	87	94.5	938	942	Score
8.6	8.6	8.6	8.6	8.6	8.6	8.6	8.6	8.6	8.8	8.9	8.9	8.9	8.9	8.9	8.9	9.0	9.2	9.2	9.2	10.0	99.6	100.0	Query Match Length
349	349	349	349	349	349	349	349	349	923	411	349	349	349	349	338	265	332	331	924	153	172	172	
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ADU86448	ADO22234	ADO08170	ADA27223	ADA27234	ADA27225	AAE34044	ABU55890	AAE12982	AAR61136	ADX93641	AED95375	ADU86486	ADS31850	AAE12983	ADF04364	AAW98720	AEB37544	AEB40857	AAE38266	ADA32883	ADC16593	ADC16591	ID
Adu86448 Human win	Ado22234 Human WNT	Ado08170 Human Wnt	Ada27223 Human NOV	Ada27234 Human NOV	Ada27225 Human NOV	Aae34044 WNT-7B pr	Abu55890 Human WNT		Aar61136 Plant bli	Adx93641 Plant ful	Aed95375 Mouse Wnt	Adu86486 Mouse win	Ads31850 Mouse win	Aae12983 Murine Wn	Adf04364 Bacterial	Aaw98720 H. pylori	Aeb37544 L. pneumo	Aeb40857 L. pneumo	Aae38266 Rice dise	Ada32883 Acinetoba	Adc16593 Scytalone	Adc16591 Scytalone	Description

Query Match

100.0%;

Score 942;

DB

7;

Length 172;

Sequence 172 AA;

The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase amino acid sequence.

Claim 1; SEQ ID NO 2; 50pp; Japanese.

Gene encoding for scytalone dehydrogenase (SCDH), useful for SCDH inhibitors and evaluating sensitivity to them.

for screening

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349 10 4 1239 8 A 4 1239 8 A 4 1066 7 A 3 119 7 A 3 3 485 5 A 3 3 485 5 A 3 3 485 5 A 3 3 7 7 A 1 1 583 7 A 1 1 1 583 7 A 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.6 349 10 AED95373 .6 449 8 ADQ79686 .6 449 8 ADQ79686 .6 1239 4 ABB58303 .4 702 8 ADS45044 .4 1066 5 ABP65862 .3 116 7 ADB31190 .3 485 5 AAB24847 .3 371 5 ABR38848 .2 370 7 ADD46192 .2 370 7 ADD46192 .2 700 7 ABD6326 .1 834 7 ADC07804 .1 227 6 ABU11390 .1 583 7 ADC68369 .1 583 7 ADC68369 .1 583 7 ADC68369 .1 583 9 AEB63072 .1 583 9 AEB03072 .1 1073 5 ABP73320 .1 1073 5 ABP73320 .1 1073 5 ABP73320 .1 1073 ADC68369 .1 1074 ADC68369 .1 1075 ABP73320 .1 1075 ABP73320 .1 1076 ADC68369 .1 1076 ADC68	75	75.5	75.5	75.5	75.5	76	76	76	76	76	76.5	77	77.5	77.5	78.5	78.5	79	79	79.5	81	81	(
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10 AED95373 . AD079686 4 ABE58303 3 8 AD545044 4 ABE58303 8 AD545047 7 ADE31326 7 ADD46192 7 AD061326 7 ADC07804 ABUI1390 5 ABE63366 7 ADC68366 7 ADC68366 7 ADC68366 7 ADC68367 7 ADC68367 7 ADM5547 9 AEC88477	5	496	36946	591	430	430	1073	583	583	583	227	834	700	530	371	485	119	1066	702	1239	449	349	
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	Aed95373 Adq79686 Abb58303 Ads45044 Abp65862 Ade31190 Aae248477 Abr38848 Add46192 Abo80326 Adc07804 Abu11390 Abg6960340 Abg73330 Adm05547 Adm193131 Adm978331	ABM82004	ADV97835	ADN19131	AEC88477	ADM05547	ABP73320	AEB03072	ADC68369	ABG69062	ABU11390	ADC07804	ABO80326	ADD46192	ABR38848	AAE24847	ADE31190	ABP65862	ADS45044	ABB58303	ADQ79686	AED95373 ·	

ALIGNMENTS

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N-PSDB; ADC16590.
                                                                                                                  Kaku K, Watanabe S,
                                                                                                                                           12-MAR-2002; 2002JP-00066955.
                                                                                                                                                       24-FEB-2003; 2003WO-JP001980.
                                                                                                                                                                    18-SEP-2003
                                                                                                                                                                                WO2003076628-A1.
                                                                                                                                                                                           Magnaporthe grisea.
                                                                                                                                                                                                        Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
                                                                                                                                                                                                                    Scytalone dehydrogenase #SEQ ID
                                                                                                                                                                                                                                 18-DEC-2003
                                                                                                                                                                                                                                            ADC16591;
                                                                                                                                                                                                                                                         ADC16591 standard; protein; 172
                                                                                                                              (TSUB ) KUMIAI CHEM IND CO LTD.
                                                                                                       2003-748394/70.
                                                                                                                                                                                                                                (first entry)
                                                                                                                  Kawai K,
                                                                                                                   Shimizu T,
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                                                                                                                   Nagayama K;
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RESULT 2
ADC16593
ID ADC16593
ID ADC16593
ADC165
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 4; 50pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene encoding for scytalone dehydrogenase (SCDH), for SCDH inhibitors and evaluating sensitivity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
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                                                                                                                                                                                                                                                                                                                              Sequence 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaku
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for SCDH inhibitors and evaluating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-748394/70
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                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPAEEFVGMVSSKQMLGDPTLRTQHF1GGTRWEKVSEDEV1GYHQLRVPHQRYKDTTMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
     MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                    MPABEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                                                                                           MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                                                          MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase
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                                                                                                                                                                                                                                             99.6%;
99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172
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                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                Score 938; DB 7;
Pred. No. 3.3e-95;
1; Mismatches (
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Mismatches 0;
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                                                                                                                                                                                                                                                                      Length 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for screening them.
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Matches 31
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                                                                                                                                                                                                                                               A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agente for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant biocontrol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA32883
                                                                                                                                                                                                          Sequence 153
                                                                                                                                                                                                                                                                                                    The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6562958-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter baumannii protein #44.
                                                                                                                                                                                                                                    baumannii protein.
                                                                                                                                                                                                                                                                                                                                                                    Example;
                                                                                                                                                                                                                                                                                                                                                                                                          vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter baumanii proteins and nucleic acids, useful as reagents diagnosing a bacterial disease, as components of antibacterial cines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-576092/54.
                          135
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118
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                                                                                                                                                                       Similarity
                           Y--KKIDGVWKFAGL
                                                                            MLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHW 134
                                                                                                      DYHRILEVITRFQLVFDQKNWDAFDELLADQLEVDYLQFRGEPLCVVSCHEYKG--SRQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
FTLAKQQGIWKITGI 132
                                                    ALSH--LRLQHNLSNP-LIRIEQDQA----WLECNYQIYR----FSENDYFHSFGRYY
                                                                                                                               DYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQ
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4170; 328pp; English
                                                                                                                                                         Conservative
                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              baumannii.
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                                                                                                                                                                     10.0%;
                                                                                                                                                         28;
                                                                                                                                                        Score 94.5; D
Pred. No. 0.06
28; Mismatches
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                                                                                                                                                                                  Length 153;
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RESULT 4 AAE38266

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Matches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid from Oryza sativa, useful for altering abiotic stress tolerance, pathogen or disease resistance or the grain quality, nutritional content or yield in a plant.
                                                L. pneumophila protein SEQ ID NO 5189
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 924 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-2001; 2001US-0334501P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza gativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rice;
Legionella pneumophila
                        detection;
                                                                          08-SEP-2005
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                                                                                                                      AEB40857 standard; protein;
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                                                                                                                                                                                    760
                                                                                                                                                                                                                                   708 VQAYVARFYPDADSVAGDEELQ-
                                                                                                                                                                                                                                                                                 654 DKLWRFDTEALPAD----LVRRGMAEEDPT--AEHGLKLAIEDYPFANDGLLIWDAIKTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Page 133-137; 223pp; English.
                                                                                                                                                                                                                                                                                                        55 DKLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFI------GGTRWEKV---
                                                                                                                                                                                                                                                                                                                                 34;
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                                                                                                                                                                                   HTLTTIVWVAAAHHAAVNFGQYDFGGYF
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                       infection; Antibacterial; Vaccine
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Rusniok C,
Jarraud S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface proteins, are targets for identification of inhibitors. (II), vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II). (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of
                                           WO2005049642-A2
                                                                      Legionella pneumophila.
                                                                                                 detection; infection; Antibacterial; Vaccine
                                                                                                                            L. pneumophila protein SEQ ID
                                                                                                                                                          08-SEP-2005
                                                                                                                                                                                       AEB37544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 5189; 660pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genome of Legionella pneumophila Paris strain and polypeptides, useful for detection or identification
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22.8%; Pred. No. 1.3
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rusniok C,
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(UYLY-)
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24-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 1876; 660pp; English.
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                                                                                                                                                                                                                                                                                                                       Helicobacter infection; gastroduodenal disease; gastritis;
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buchier C,
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             97US-00833457
97US-00881227
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter polynucleotides - used to develop products for
the diagnosis, prevention and treatment of Helicobacter infections and
gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                           Bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 1521-1522; 2054pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-542293/46.
               N-PSDB; ADF00192
                                                         Breton
                                                                                                               09-APR-1999;
                                                                                                                                            05-APR-2000;
                                                                                                                                                                          12-AUG-2003.
                                                                                                                                                                                                                                  Proteus mirabilis
                                                                                                                                                                                                                                                                              Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                      12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                 ADF04364;
                                                                                                                                                                                                                                                                                                                                                                                             ADF04364 standard; protein; 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kleanthous H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1997;
                              WPI; 2003-895291/82
                                                                                                                                                                                                       US6605709-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                 immunostimulant.
                                                                                      (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 DEKDTFNFAKIGYEQGKGEELKEVEEK------HAFKKIPFVKDLHKIAPTI 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 FYQFVG-----FSDSCKNRRRXRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                         £,
                                                                                      GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSK-----DEVIGNPTLRTQHFIGG--TRWEKVSE-----DEVIGYHQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 AA;
                                                                                                                                                                                                                                                                                                        polypeptide #477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                              2000US-00543681
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00902615
                                                                                                                 99US-0128706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 85; DB 2; Length 265; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller C,
                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomb J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oomen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to new Proteus mirabilis polypeptides and polypucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polypucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                           lung fibrosis; skeletal disorder; platelet disorder; cell proliferation; transplant rejection; acquired immune deficiency syndrome; AIDS; wound; connective tissue disease; drug screening; ulcer; liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                Mouse; Wnt-7B-like protein; gene therapy; hypotensive; neoplasia; cancer; tranquillizer; inflammatory disorder; arthrittis; haematopolesis; allergy; immune disorder; autoimmune disease; thyroiditis; restenosis; thrombosis; neurological disease; Alzheimer's disease; cardiovascular disorder; burn; diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis; rheumatoid arthritis; thrombocytopaenia; skin disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                           03-APR-2000; 2000US-0194256P.
26-JUL-2000; 2000US-00625634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine Wnt-7B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4649; 870pp; English.
    Vernet CAM,
                                                                                                                                    03-APR-2001; 2001WO-US010679.
                                                                                                                                                                                                                 WO200174856-A2
                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12983 standard; protein;
                                          (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 -----WGEF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 GI---ÈII--ERLKAQGRNVIFMVPHGWAVDVPAMLLAAKGQKMAAMFHHQKDPVTDYLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 NKARYHFGGRLHSREAGIKPFISTVROGFWGYY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 KVSEDEVIGYHQLR------VPHQRYKDTTMKEVTMKGHAHSANLHWYKK--IDGVW 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 WDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLR-TQHFIGGTRWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDKAQR-----EDVLDKMFETAP-QSFV-----MLADLCLRGAKHTLQRTSWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
  Rastelli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9%; Score 84; DB 7;
25.5%; Pred. No. 2.6;
    Herrmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 10
ADS31850
ID ADS31
XX
AC ADS31
XX
DT 30-D
TX
DT 30-D
XX
MOUS
XX
Whit
KW Whit
KW Whit
KW Whit
KW Whit
XX
OS MUS
XX
OS MUS
XX
PN WO:
XX
PD 14
XX
PF 26
XX
PF 26
XX
PR 27
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, carquired immune deficiency syndrome (AIDs), transplant rejection, allergy, infection, inflammatory disorder, arthritis, haematopoietic disorder, skin disorder (keloid), restenosis, neurological disease, compared to the disorder section, restenosis, neurological disease, and cardiovascular disorders such as diabetes mellitus, atherosclerosis, cerebral thrombosis or haemorrhage, and other diseases, including cerebral thrombosis or haemorrhage, and other diseases, including hypertension, hypothyroidism, myeloid or lymphoid cell deficiencies and rarious platelet disorders such as thrombocytopaenia. Wmi-7B-like protein compared to useful for cell proliferation, tissue repair and in the treatment of burns, incisions and ulcers, periodontal disease and treatment of lung or liver fibrosis. Wmi-7B-like protein plays an important role in continuation of tumour growth, chemoresistance, radiotherapy resistance and also for screening drugs. Wmi-7B-like nucleic acids are useful in gene therapy. The present sequence is murine Wmi-7B protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Wnt-7B-like polypeptides and polynucleotides for diagnosing, preventing and treating broad range of pathological states such as cancer, hematopoietic, inflammatory, skin, skeletal disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                     vulnerary; cell therapy; cartilage formation;
fibroblast growth factor 18; FGF-18; sonic hedgehog; Shh; beta-catenin;
Wnt; tissue repair; tissue reconstructon; airway; trachea; bronchi; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Fig 2B; 115pp; English
                                                                                                                                                                     WO2004087055-A2
                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                          Mouse wingless Wnt7b.
                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS31850 standard; protein; 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, i
disorder, autoimmune diseases, such as connective tissue disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating and preventing Wnt-7B-like-associated disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human Wnt-7B-like protein and its cDNA molecule. Human Wnt-7B-like proteins and their nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis.
                                                                                                                                                                                                                                                      larynx; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-626382/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%; Score 84;
31.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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27-MAR-2003; 2003US-0458224P 26-MAR-2004; 2004WO-US009264.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT

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RESULT 11
ADU86486
ID ADU866
XX ADU86
XX ADU86
XX ADU86
XX ADU86
XX MOUS6
XX WAIT;
KW PARK;
KW PARK;
KW MOLOZ
XX MUS TO
XX MO200
PN WO200
PN WO200
PF 17-MP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence encoding at least one cartilage formation inducing protein (CC consisting of FGF-18, Shh, beta-catenin or Wmt proteins; expressing FGF-CC 18 protein in a cell in vitro; treating a patient in need of cartilage (CC formation in an affected area of the patient; a cell culture comprising (CC cells, in a medium capable of sustaining cell growth, having an (CC expression vector comprising at least one mucleotide sequence encoding at (CC east one cartilage formation inducing protein consisting of FGF-18, Shh, (CC cells capable of inducing cartilage formation in vitro in a medium (CC capable of sustaining cell growth The pharmacutical composition is useful in inducing cartilage formation in vitro in a medium (CC capable of sustaining cell growth The pharmacutical composition is useful in inducing call growth (CC capable of sustaining cell growth) (CC various tissues in a conducting airway, e.g., trachea, bronchi, lung or (CC various tissues in a conducting airway, e.g., trachea, bronchi, lung or (CC various tissues in a conducting airway, e.g., trachea, bronchi, lung or (CC larynx of a patient. This is the amino acid sequence of mouse whith.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                least one cartilage formation inducing protein consisting of fibrobla growth factor (FGF)-18, sonic hedgehog (Shh), beta-catenin or Wnt proteins to induce cartilage formation. Also described are: inducing cartilage formation in an affected area of a patient requiring such treatment; an expression vector comprising at least one nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New pharmaceutical composition comprising a cartilage formation inducing protein, e.g., fibroblast growth factor (FGF)-18, sonic hedgehog (Shh), beta-catenin or Wnt proteins, useful in repairing tissues in a conducting
                                                                                                                                                                                                                     Wnt; wingless-type protein; neurogenesis; spinal cord injury; injury; parkinsons disease; antiparkinsonian; neurological disease;
                                                                                                                                                                                                                                                                                   Mouse wingless-type protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 14; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-729163/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whitsett
                                17-MAY-2004; 2004WO-US015264
                                                                          02-DEC-2004.
                                                                                                                   WO2004103394-A2
                                                                                                                                                                                                                                                                                                                                                                                                               ADU86486 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a new pharmaceutical composition comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                    neurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS31849.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                  disease; neuroprotective; paralysis.
                                                                                                                                                                                                                                                                                                                                                                                                             protein; 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                     Wnt7B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 349;
2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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Best Local (
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                                                                                                                                                                                                                                                                                                                             growth of a neuron, a pharmaceutical composition for modulating growth of a neuron in a mammal (comprising a Wnt, a Wnt-like substance, or a chemical compound affecting a Wnt signaling pathway and a pharmaceutical preparation suitable for delivery to the mammal) and a method of inhibiting growth of a neuron in a subject. The neuron is a neuron in a spinal cord that has been damaged by traumatic spinal cord injury. Inhibiting growth of a neuron in a subject comprises providing a composition (comprising a secreted frizzled-related protein (sFRP), sFRP-like substance, Ryk or Ryk-like substance and a pharmaceutical preparation suitable for delivery to the subject and administering the composition to the subject. sFRP and Ryk are both proteins that bind to block the activity of Wnt. The method is useful for modulating growth of a neuron for preparing a composition for treating spinal cord disorder, paralysis, Parkinson's disease and motor neurone disease. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to modulating growth of a neuron comprises contacting the neuron with a Wnt (wingless-type protein), a Wnt-like substance, and/or a chemical compound affecting a Wnt signaling pathway. Also included are a method for identifying a substance that modulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating growth of a neuron for treating spinal cord disorder or paralysis comprises contacting the neuron with a Wnt, a Wnt-like substance, and/or a chemical compound affecting a Wnt signaling pathway.
                                                                                                                                                                                                                                                                   Sequence 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 60; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYCH-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2003; 2003US-0470913P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-834171/82
131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                           134 -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                       74
                                                                                                                                   84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                              32;
                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV CHICAGO
                                                                                         QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
                                                                                                                                                                                                                                                                                                             represents a Wnt protein from human or mouse
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                      AA,
                                                                                                                                                                                                   8.9%;
                                                                                                                                                                            11;
                                                                                                                                                                                                 Score 84; DB 8; Length 349; Pred. No. 2.7;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                 36;
                                                                                                                                                                                 Indels
                                                                                                                                                                                 24;
                                                                                                                                                                              Gaps
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RESULT 12
ARD95375
ID ARD95375
AC AED95
XX AED95
XX AED95
XX Cell
CW Cell
KW antia
KW ather
KW ather
KW cardi
XX Card
XX Cardi
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell proliferation; cell regeneration; Wnt signaling pathway; cardiant; antiarteriosclerotic; vasotropic; cytostatic; myocardial infarction; atherosclerosis; coronary artery disease; myocardial disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Wnt7B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AED95375 standard; protein; 349 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AED95375;
                                                                                                                                                                                                                                                                                                                                                         US2005261189-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heart disease; cancer; Wnt7B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:46.
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18-APR-2005; 2005US-00108528

24-NOV-2005.

16-APR-2004; 2004US-0563137P 02-AUG-2004; 2004US-0598368P

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RESULT 13
ADX93641
ID ADX93
XX
AC ADX93
XX
AC ADX93
XX
DT 21-AF
XX
DE Plant
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC the cell with a composition comprising an agent that acts at the cell with a composition comprising an agent that acts at the cell with a consposition comprising an agent that acts at the cell composition composition composition to promote cell where the cell is contacted with an amount of the composition to promote composition to adult cardiac cell proliferation and/or regeneration. Also described: (1) treating a condition having cardiac cell injury or death; (2) treating a developmental disorder of cardiac cell; and (3) a conditied polypeptide comprising a Wnt-related polypeptide or bioactive fragment, where the modified Wnt-related polypeptide or bioactive fragment, where the modified Wnt-related polypeptide or bioactive fragment, where the wnt promoting cardiac cell proliferation and/or regeneration, where the Wnt propertide or bioactive fragment is useful in the manufacture of a medicament for promoting cardiac cell proliferation and/or regeneration, where the Wnt propertide or bioactive fragment is modified with one or more moieties to produce a conditied wnt polypeptide or bioactive fragment. The method is useful for composition meanufacture fragment. The method is useful for cell injury or death, e.g. myocardial infarction, atherosclerosis, cell injury or death, e.g. myocardial infarction, atherosclerosis, coronary artery disease, obstructive vascular disease, dilated coronary artery disease, obstructive vascular disease, valvular heart cell repetiting from cancer or cancer related conditions such as structural ceropresents mouse wnt7B, which is used in the exemplification of the ventral invention. Mouse wnt7B is located on chromosome 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 32
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                              Plant full length insert polypeptide segid 56305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 46; 203pp; English
                                                                                                         21-APR-2005
                                                                                                                                                                                 ADX93641;
                                                                                                                                                                                                                                             ADX93641 standard; protein; 411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for promoting neonatal or adult cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENBANK; NM_009528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYDR-) HYDRA BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2006-008454/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                  : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຸດ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
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                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9%; Score 84; DB 10;
31.1%; Pred. No. 2.7;
tive 11; Mismatches 36
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                                                                                                                                                                                                                                                                                                                                                                                                                       -WKWGGCSADVRYG-IDFSRRFVDARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The method comprises contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shamah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                                                                                                                                                                                                                                             New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 56305; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIUJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-2003; 2003US-00425114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                improving yield
                                                                                                                                                                                                                                                                                                                                                                                                              Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TABA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ZHOU Y.
) KOVALIC D K.
) SCREEN S E.
) TABASKA J E.
) CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                              Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIU J.
                                                                                                                                                                                                                                                                                                                                                                                                              Kovalic
                                                                                                                                                                                                                                                                                                                                                                                                              DK,
                                                                                                                                                                                                                                                                                                                                                                                                              Screen SE,
                                                                                                                                                                                                                                                                                                                                                                                                              Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                              Cao
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or

plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the invention.

Sequence 411 AA;

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                                                                                                                                         Matches
                                                                                                                                                      Query Match
Best Local
131 NLHWYKKIDGVWKFAGLKP 149
                                                     71
                                                                                                            26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF-----LDK----LW-EAMPAEEFVGMV
                                                                                                                                         35;
                                                                                                                                                       Similarity
                         ----SKWQQVL---
                                                     SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
                                                                                 WKDVFDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM-
                                                                                                                                         Conservative
                                                                                                                                                      8.9%; Score 84; DB 25.2%; Pred. No. 3.4;
                                                                                                                                       17;
                                                                                                                                         Mismatches
                          -YHWLCSPNPDFNEI-
                                                                                                                                                                  8;
                                                                                                                                       31; Indels
                                                                                                                                                                  Length 411;
                                                                                                                                       Gaps
                                                                                                              70
                            256
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RESULT 15
AAB12982
ID AAB12
XX AAB12
AC AAB12
XX 28-JA
XX 28-JA
XX Human
XX Human
XX Human
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AAR61136
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Best Local S
Matches 34
         Human; Wnt-7B-like
                                                                                                       AAE12982 standard;
                                                                                                                                                                                                                                                                                                                                                                      Sequence 923
                                                                                                                                                                                                                                                                                                                                                                                           animal or plant cells specific lipoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                   The cDNA encoding the blight resistance-specific lipoxygenase (See AAQ68842) is useful for the elucidation of the mechanism of blight resistance in plants and makes possible the expression of various proteins in the chloroplast. The cDNA may also be expressed in back
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 5-11; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant blight resistance-specific lipoxygenase gene - useful for expression of proteins in the chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ68842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant blight-specific resistance lipoxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR61136 standard; protein;
                             Human Wnt-7B-like protein from clone 29518614.0.61.
                                                         28-JAN-2002
                                                                                AAE12982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO
                                                                                                                                                                                                                                                                                                              Local L
                                                                                                                                                                   761 LTNIVWVAAAHHAAVNFGQYDFGGYF 786
                                                                                                                                                                                                                                                                      653
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                                                                                                                                                                                                                    709 AYVARFYPDADSVAGDEELQ-----AFWTEVRTKGHGDKKDAPWWPKLDSPESLAHT
                                                                                                                                                                                                                                                                                             55 DKLW----EAMPAEEFVGMVSSKQMLGDPT-----LRTQHF----IGGTRWEKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                                                                                                      DKLWRFDTEALPAD----LVRRGMAEEDPTAEQGLKLAIEDYPFANDGLLIWDAIKTWVQ
                                                                                                                                                                                             ----VWKFAGLKPDIRWGEFDFDRIF
                                                                                                                                                                                                                                             -----SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG-----
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                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                         (first
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                                                                                                       protein;
                                                                                                                                                                                                                                                                                                                                8.8%;
       protein;
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                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                      oplast. The cDNA may also be expressed in bacterial, to recombinantly produce the blight resistance-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant production.
                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                     Score 83; DB Pred. No. 13; 16; Mismatches
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                                                                                                         349 AA
       gene
      therapy; hypotensive;
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                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                             Length 923;
                                                                                                                                                                                                                                                                                                                      Indels
       neoplasia;
                                                                                                                                                                                                                                                                                                                      50;
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tranquillizer; inflammatory disorder; arthritis; haematopoiesis; allergy; immune disorder; autoimmune disease; thyroiditis; restenosis; thrombosis; neurological disease; Albeimer's disease; cardiovascular disorder; burn; diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis; rheumatoid arthritis; thrombocyropaenia; skin disorder; atherosclerosis; lung fibrosis; skeletal disorder; platelet disorder; cell proliferation; transplant rejection; acquired immune deficiency syndrome; AIDS; wound;
                                                                                          03-APR-2001; 2001WO-US010679.
03-APR-2000;
                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                               WO200174856-A2
                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                connective tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; drug screening; ulcer; liver fibrosis
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26-JUL-2000; 2000US-0194256P. 2000US-00625634.

(CURA-) CURAGEN CORP

Vernet CAM, Rastelli Ļ Herrmann

2001-626382/72.

New Wnt-7B-like polypeptides and polynucleotides for diagnosing, preventing and treating broad range of pathological states such as cancer, hematopoietic, inflammatory, skin, skeletal disorders and atherosclerosis.

Claim 12; Fig 2A; 115pp; English.

Alzheimer's disease, trauma, wound, spinal cord injury, skeletal disorder and cardiovascular disorders such as diabetes mellitus, atherosclerosis, cerebral thrombosis or haemorrhage, and other diseases, including hypothyroidism, myeloid or lymphoid cell deficiencies and various platelet disorders such as thrombocytopaenia. Wnt-7B-like protein is also useful for cell proliferation, tissue repair and in the treatment of burns, incisions and ulcers, periodontal disease and treatment of lung or liver fibrosis. Wnt-7B-like protein plays an important role in autocrine stimulation of tumour growth, chemoresistance, radiotherapy resistance and also for screening drugs. Wnt-7B-like nucleic acids are useful in gene therapy. The present sequence is human Wnt-7B-like protein which is obtained from clone 29518614.0.61 The invention relates to human Wnt-7B-like protein and its cDNA molecule. Human Wnt-7B-like proteins and their nucleic acids are useful for treating and preventing Wnt-7B-like-associated disorders such as neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, immune disorder, autoimmune diseases, such as connective tissue disease, multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, acquired immune deficiency syndrome (AIDS), transplant rejection, allergy, infection, inflammatory disorder, arthritis, haematopoietic disorder, skin disorder (keloid), restenosis, neurological disease,

Sequence 349 A,

Similarity

8.6%;

DB 4;

Length 349;

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Best Local S
Matches 30
 138
                      134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                81
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                                                                                                  30;
GYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                       RW--EKVSEDEVIGYHOLRVPHORYKDTTMKEVTMKGHAHS-----ANLH------
                                                RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137
                                                                                                  Conservative
                                                                                                  11;
                                                                                                Score 81; DB 'Pred. No. 5.8;
                                                                                                31;
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Search co completed: December ç 2006, 01:22:15 This Page Blank (uspto)

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                       1 MGSQVQKSDEITFSDYLGLM......WGEFDFDRIFEDGRETFGDK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Q3ie87 pseudoalter	Q5wyb7 legionella		ω	7	. Q7tdf4 halovirus h	Q9rb47 clostridium	nocardia	Q8zsd9 anabaena sp	Q5bh35 aspergillus		Q8njh9 ophiostoma	Q8nji3 ophiostoma				Q8njil ophiostoma						Q8nji5 ophiostoma		Q			Q9c426 ophiostoma		Q6xrll ceratocysti	na	Description	

ALIGNMENTS

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X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS). X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS). MEDLINE=99310043, PubMed=10382670; DOI=10.1002/(SICI)1097-0134(19990601)35:4<425::AID-PR Wawrzak Z., Sandalova T., Steffens J.J., Basarab G.S. Lindqvist Y., Jordan D.B.; "High-resolution structures of scytalone dehydratase- complexes crystallized at physiological ph."; Proteins 35:425-439(1999).	X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS). MEDLINE=99119201, PubMed=9922139; DOI=10.1021/bi981848r; MEDLINE-99119201, PubMed=9922139; DOI=10.1021/bi981848r; Chen J.M., Xu S.L., Wawrzak Z., Basarab G.S., Jordan D.B.; "Structure-based design of potent inhibitors of scytalone displacement of a water molecule from the active site."; Biochemistry 37:17735-17744 (1998).		Biosci. Biotechnol. Biochem. 62:564-566(1998). [2] X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS). MEDLINE=95171111; PubMed=7866745; Lundqvist T., Rice J., Hodge C.N., Basarab G.S., Pierce J., Lindqvist Y.; "Crystal structure of scytalone dehydratase a disease of the rice pathogen, Magnaporthe grisea."; Structure 2:937-944(1994).	NUCLEDITIDE SEQUENCE [MRNA]. MEDLINE=98233280; PubMed=9571787; MOTOYama T., Imanishi K., Yamaguchi I.; "CDNA cloning, expression, and mutagenesis of scytalone needed for pathogenicity of the rice blast fungus, Pyric oryzae.";	RESULT 1 SCYD MAGGR SCYD MAGGR STANDARD; PRT; 172 AA. AC P56221; DT 15-UUL-1998, integrated into UniProtKB/Swiss-Prot. DT 15-UUL-1998, sequence version 1. DT 07-FEB-2006, entry version 34. DT 07-FEB-2006 entry version 34. DE Scytalone dehydratase (EC 4.2.1.94). GN Name=Sdh1; OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea). OC Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycete OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe DX NCBI TaxID=148305;
., Lundqvist T., inhibitor	8r; D.B.; ilone dehydratase: e.";	(1b; complex of tight-binding binding	Ф	lone dehydratase Pyricularia	grisea). omycetes; aporthe.

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RESULT 2
Q6KR11 9PEZI
ID Q6KR11_9PEZI PRELIMINARY; PRT; 186 AA.
AC Q6KR11;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
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Distributed under the Creative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scytalone they are to yield melanin.
- CATALYTIC ACTIVITY: S
H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homotrimer. Each subunit contain the central part of the hydrophobic functions independently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1IDP; X-ray;
2STD; X-ray;
2STD; X-ray;
3STD; X-ray;
4STD; X-ray;
5STD; X-ray;
6STD; X-ray;
5STD; X-ray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                       ro; IPR004235; SCY-
ro; IPR004235; Scytalone_dh; 1.
PF02982; Scytalone_DH; 1.
m; PD022193; Scytalone_DH; 1.
PO22193; Scytalone_DH; 1.
Scytalone_dehydratase.
/FTId=PRO_0000097639.
                                                                                        121
                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB004741; BAA34046.1; -; mRNA.
LIDP; X-ray; A/B/C=1-172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF02982;
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                                                                                                                           61
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                                                                                                                                                                                           Similarity
                                                                                 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK
                                                                                                                     MPAEEFVGMVSSKOMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                                                                                                                                         MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                          MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                                                                                                                              MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                       VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fungal melanin biosynthesis; first step.
Homotrimer. Each subunit contains an active site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catalyzes two steps in melanin biosynthesis. they are two dehydration steps and one reduct
                                                                                                                                                                                                                     ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A/B/C=10-172.

A/B/C=10-172.

A/B/C=10-172.

A/B/C=10-172.

A/B/C=10-172.

A/B/C=10-172.
                                                                                                                                                                                                                               20250 MW;
                                                                                                                                                                                         99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scytalone =
                                                                                                                                                                                Score 938; DB 1
Pred. No. 3e-77;
1; Mismatches
                                                                                                                                                                                                                      2FA56296D5EE00DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,3,8-trihydroxynaphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      see http://www.uniprot.org/terms
Attribution-NoDerivs License
                                                                                                                                                                                                  1; Length 172;
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RESULT 3
SCYD_GLOLA
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Matches 118
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15-JUL-1998,
01-NOV-1996,
07-FEB-2006,
                                                                                                                                                                                    lagenarium).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                                                                                                                                        SCYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02982; Scytalone dh; 1.
ProDom; PD022193; Scytalone DH;
SEQUENCE 186 AA; 21516 MW; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceratocystis resinifera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004, sequence version 07-FEB-2006, entry version 7. Syctalone dehydratase I.
                                                            MEDIINE=97111971; PubMed=8953707;
Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa l
"Cloning and structural analysis of the melanin biosynthesis
encoding scytalone dehydratase in Colletotrichum lagenarium.'
Appl. Environ. Microbiol. 62:4340-434(1996)
-!- FUNCTION: Catalyzes two steps in melanin biosynthesis. Fi
scytalone they are two dehydration steps and one reduction
                                                                                                                                                                                                                                                    Glomerella lagenarium
                                                                                                                                                                                                                                                                 Name=SCD1;
                                                                                                                                                                                                                                                                          07-FEB-2006, entry version 28.
Scytalone dehydratase (EC 4.2.1.94).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016836; F:hydro-lyase activity; IEA.
GO; GO:0006582; P:melanin metabolism; IEA.
InterPro; IPR004235; Scytalone_DH.
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PATHWAY:
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                                     scytalone they are yield melanin. CATALYTIC ACTIVITY.
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nilarity 72.8%;
Conservative 2:
  Homotrimer.
                                                                                                                                                                                                                                                                                                    sequence version
               Fungal melanin
                                                                                                                                                                                                                                                                                                               integrated into UniProtKB/Swiss-Prot
                                     ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene
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Pred. No. 2.4e
21; Mismatches
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  subunit
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   contains an
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   active
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                                                                                                                            Furusawa I.;
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Best Local Sim
Matches 115;
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Q9C426 OPHFL
Q9C426;
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Pfam; PF02982; Scytalone_Dh; 1.
ProDom; PD022193; Scytalone_DH; 1.
Lyase; Melanin biosynthesis.
    HSSP; P56221; 1IDP.

SMR; 09C426; 22-182.

GO; GO:0016836; F:hydro-lyase activity;
GO; GO:0006582; P:melanin metabolism; IF
InterPro; IPR004235; Scytalone_DH.
Pfam; PF02982; Scytalone_dh; 1.
Pf02982; Scytalone_dh; 1.
                                                                                                                                                                                                                                                 "A scytalone dehydratase gene from Ophios melanization and pathogenicity phenotypes Colletotrichum lagenarium mutant,";
                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                         Ophiostoma floccosum
                                                                                                                                                                                                                                                                                                                                                                                                                                    Scytalone dehydratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001, integrated into 0
01-JUN-2001, sequence version
07-FEB-2006, entry version 12
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HSSP; P56221; 1IDP.
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                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                 Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                       MO1.
                                                                                              EMBL; AF316575; AAK11296.1; -;
                                                                                                                                                                                              STRAIN=387N;
                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                             Wang H.L., Kim S.H.,
                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                          MEDLINE=21473268; PubMed=11589570; DOI=10.1007/s004380100534;
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                                                                                                                                                                                Breuil C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NMHWYRKVNGVWKFAGLNPEIRWSEYDFDAVFADGRDSYG
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  Scytalone_DH; 1
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71.9%;
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Pred. No. 3e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016836; F:hydro-lyase activity; GO; GO:0006582; P:melanin metabolism; IEInterPro; IPRO4235; Scytalone DH. Pfam; PF02982; Scytalone dh; 1. ProDom; PD022193; Scytalone DH; 1. SEQUENCE 185 AA; 21285 MW; EB9937DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, functional analysis and expression of a scytalone dehydratase gene ( SCD1) involved in melanin biosynthesis ophytopathogenic fungus Bipolaris oryzae.";
Curr. Genet. 45:197-204(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bipolaris oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
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07-FEB-2006, entry version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kihara J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=14716498; DOI=10.1007/s00294-003-0477-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=D9/F6-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moriwaki A., Ueno M., Tokunaga T., Arase S.,
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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67.5%;
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                                                                                                                                                                                                                                                                                                                             Score 657; DB 2;
Pred. No. 1.3e-51;
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Pred. No. 3.5e-54;
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RESULT

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O75BEI NEUCR
ID O75BEI NEUCR
AC O75BEI NEUCR
DT 15-DEC-2003, i
DT 15-DEC-2003, i
DT 07-FBB-2006, e
DE Hypothetical |
DE Hypothetical |
DE OFFNames=NCUO7
OS Neurospora cra
OC Eukaryota; Fur
OC STRAIN=74-OR2
RN (1]
RN NUCLEOTIDE SER
RC STRAIN=74-OR2
RX MEDLINE=22598
RA Jaffe D. Fit
RA Jaffe D. Fit
RA Galagan J.E.,
RA Galagan J.E.,
RA Warner-Washbu
RA Galagan J.E.,
RA Warner-Homan
RA Warner-Homan
RA Warner-Toman
RA Warner-Toman
RA Marcotte E., E
RA Warner-Toman
RA Marcotte E., E
RA Warden O., Pil
RA Marcotte E., E
RA Marcot
RESULT 7
Q8NJI6 9PEZI
ID Q8NJI6 9
AC Q8NJI6;
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RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A., Braun E.L.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Machine E., Bielke C., Rudd S., Frishman D., Krystofova S.,
RA Machine G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A.,
RA Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A.,
RA Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A.,
RA Marcing D.O., Alex L.A., Mannhaupt G., Radford A., Aramayo R.,
RA Varden O., Plamann M., Seiler S., Nusbaum C., Birren B.W.,
RA Marvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.,
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868 (2003).

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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Sordariomycetidae; Sordariales
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
ORFNames=NCU07823.1;
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                                 QBNJI6 9PEZI
QBNJI6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMR; Q7SBE1; 11-171.

GO; GO:0016836; F:hydro-lyase activity; IEA.

GO; GO:0006582; F:melanin metabolism; IEA.

Interpro; IPR004235; Scytalone_DH.

Pfam; PF02982; Scytalone_DH; 1.

ProDom; PD022193; Scytalone_DH; 1.
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      01-OCT-2002,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                  MPAEEFIKMVSDKKVIGNPLLRTQHFMSGISKWEKVSDTEIIGYHQLRVPHQVYTDSSCT
                                                                                                                                                                                                                                                                                                                                                                               MPAEEFVGMVSSKQMLGDPTLRTQHFIGG-TRWEKVSEDEVIGYHQLRVPHQRYKDTTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANAANPEKRITFEEYLGCTEACFEWADSYDTKDFDRLRKCIAPTLRIDYRSFLNKLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein.
174 AA; 2
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                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 627.5; DB 2
Pred. No. 5.8e-49;
5; Mismatches 34
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         UniProtKB/TrEMBL
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                                                                   PRT;
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Best Local S
Matches 93
                  EMBL; A
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Q2WEI4;
10-JAN-2006, integrated integrated version ve
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I4 SORMA
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HSSP; P56221; 1IDP.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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                                                                                                                                                                                                                                        STRAIN=S48977; TISSUE=Mycelium;
Nowrousian M., Wuertz C., Poeggeler S., Kueck U.;
"Why sequencing of Sordaria macrospora will lead to an i
annotation of the Neurospora crassa genome.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sordaria macrospora.
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GO:0006582; P:melanin metabolism; IEA.
erPro; IPR004235; Scytalone_DH.
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   AJ575152; CAE00795.1; -;
ER 150 150
NCE 150 AA; 17348 MW;
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122 AA;
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                                                                                                                                               under the Creative
                                                                                                                                                                             by the UniProt Consortium,
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76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologue
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Pred. No. 4.4e-42;
5; Mismatches 14
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                                                                         Genomic_DNA.
                                                                                                                                               Commons
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                                                                                                                                               see http://www.uniprot.org/terms
Attribution-NoDerivs License
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CB9B307F47C1D5A7

CRC64;

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Length

150;

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RESULT 10
Q8NJI7 9PEZI
ID Q8NJI7 9PEZI
AC Q8NJI7;
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Best Local S
Matches 92
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Best Local S
Matches 98
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GBNJIS;
01-OCT-2002, integrated into Unit
01-OCT-2002, sequence version 1.
07-FEB-2006, entry version 10.
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                                                                                                                                                                                                                                                                             Pfam; PF
ProDom;
                                                                                                                                                                                                                                                                                                                                     SMR;
                                                                                                                                                                                                                                                                                                                                              EMBL; AY098657; AAM34803.1; -; HSSP; P56221; 1IDP.
                                                                                                                                                                                                                                                                                                                                                                                                              Fleet C., Breuil C.; "Fleet C., Breuil C.; "Inhibitors and genetic analysis of scytalone dehydratase presence of DHN-melanin pathway in sapstain fungi."; Mycol. Res. 106:1331-1339(2002).
                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scytalone dehydratase (Fragment).
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=104300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ophiostoma floccosum.
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GO:0006582; P:melanin metabolism; IEA.
erPro; IPR004235; Scytalone_DH.
m; PF02982; Scytalone_dh; 1.
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                                                                                                                      HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF
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                                                                                    À 145
                                                                                                         HFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKF
                                                                                                                                                     EWADRYDSKOWDRIRKCIAPTIRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLIRTQ
                                                                                                                                                                 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGWVSSKQMLGDPTLRTQ
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121 AA;
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           PRELIMINARY;
                                                                                                                                                                                                                                                                         Scytalone_DH; 1.
                                                                                                                                                                                                                                           14234 MW;
                                                                                                                                                                                                          57.7%;
76.0%;
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                                                                                                                                                                                               Score 544; DB
Pred. No. 1.5e-
L5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 548.5; DB 2
Pred. No. 7.7e-42;
1; Mismatches 30
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                           1940509D85F8A42A CRC64;
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           122
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                                                                                                                                                                                                          DB 2;
.5e-41;
           ξ
                                                                                                                                                                                                 14; Indels
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                                                                                                                                                                                                                    Length 121;
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RESULT 11
QBNJIB 9PEZI
ID QBNJIB;
AC QBNJIB;
DT 01-CCT-2002, se
DT 07-FEB-2006, en
DE Scytalone dehyd
OS Ceratocystis pi
OC QBNATOS Fung
OC Hypocreomycetis.
OC Ceratocystis.
OX NCBI_TAXID=7203
RN NCBI_TAXID=7203
RN I1
RP NUCLEOTIDE SEQU
RA Fleet C., Breui
RT "Inhibitors and
RT presence of DHN
RL Mycol. Res. 106
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DR HSSP; P56221; 1
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Matches 92
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                                                                                                                                      Fleet C., Breuil C.;
"Inhibitors and genetic analysis of scytalone dehydratase presence of DHN-melanin pathway in sapstain fungi.";
Mycol. Res. 106:1331-1339(2002).
                                                                                                                                                                                                                                                                                                                                                                                           Ceratocystis pinicola.
Eukaryota; Fungi; Ascomycota;
Hypocreomycetidae; Microascale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002, integrated into U
01-OCT-2002, sequence version
07-FEB-2006, entry version 10.
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SMR; QBNJT7; 1-122.

GO; GO:0016836; F:mydro-lyase acti
GO; GO:0006582; P:melanin metaboli
InterPro; IPR004235; Scytalone_DH.

Pfam; PF02982; Scytalone_dh; 1.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002, integrated into UniProtKB/TrEMBL 01-OCT-2002, sequence version 1. 07-FEB-2006, entry version 11.
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"Inhibitors and genetic analysis of scytalone dehydratase confirm presence of DHN-melanin pathway in sapstain fungi.";
Mycol. Res. 106:1331-1339(2002).
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                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE. Fleet C., Breuil C.;
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=72031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scytalone dehydratase (Fragment).
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Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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GG; GO:000558; P:melanin metabolism; IEA.
InterPro; IPR004235; Scytalone_HH.
Pfam; PF02982; Scytalone_dh; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Inhibitors and genetic analysis of scytalone dehydratase presence of DHN-melanin pathway in sapstain fungi."; Mycol. Res. 106:1331-1339(2002).
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Fleet C., Breuil C.;
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GO:0006582; P:melanin metabolism; IEA.
GPPTO; IPR004235; SCytalone_DH.
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Q8NIE1; 1-122.
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n; PD022193; Scytalone_DH;
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Ophiostoma piliferum.

Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Ophiostoma.
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01-OCT-2002, sequence version
07-FEB-2006, entry version 10
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QBNJI2;
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                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
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Pfam; PF02982; Scytalone_dh; 1.
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GO:0016836; F:hydro-lyase activity;
GO:0006582; P:melanin metabolism; II
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                                 analysis of scytalone dehy pathway in sapstain fungi.
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SMR; QBNJI1; 1-122.

GO; GO:0016836; F:hydro-lyase activity; IEA.

GO; GO:0006582; P:melanin metabolism; IEA.

InterPro; IPR004335; Scytalone DH.
                                                                                                                                                                                                                                                                                                        Fleet C., Breuil C.; "Fleet C., Breuil C.; "Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi."; Mycol. Res. 106:1331-1339(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                    Scytalone dehydratase (Fragment).

Ophiostoma piliferum.

Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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QBNJI1;
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InterPro; IPR004235; Scytalone_DH.
Pfam; PF02982; Scytalone_dh; 1.
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HSSP; P56221; 1IDP.
SMR; Q8NJI0; 1-121.
                                                                                                                                                                                                                        EMBL; AY098663; AAM34809.1; -; Genomic_DNA.
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                                                                                                            Pfam; PF02982; Scytalone_dh; 1.
ProDom; PD022193; Scytalone_DH; 1.
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Score 530; DB 2; L
Pred. No. 2.9e-40;
L7; Mismatches 16;
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Pred. No. 1.9e-40;
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                               DB 2; Length 122;
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Search completed: December Job time: 304 secs

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Run on: OM protein - protein search, using sw model December 5, 2006, 01:22:36; Search time 40 Seconds GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd. (without alignments)
413.732 Million cell updates/sec

Title: Perfect score: US-10-507-132-2 942

MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	ر. د	4	ω	2	ם	No.	Result
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7.9	8.0	8.0	8.0	8.0	8.0	8.1	8.1	8.1	8.1	8.2	8.2	8.2	•	8.2	8.3	8.4	8.4	8.4	8.4	8.4	8.5	٠	8.8		9.0	9.3	10.6	98.9	Match	* Query
162	1405	514	497	591	315	1150	356	356	325	479	274	816	356	299	380	702	469	265	1239	614	388	923	266	349	380	σ	605	7	Length	
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	ν	N	N	N	J-4	N	N	N	N	N	_	N	N	2	B	
н69896	T40607	B64055	T27012	S56202	JQ1250	T41260	B85867	A91023	G84362	T26951	T51714	S54518	G64997	T40437	I47176	A75630	B96947	D71838	A32579	T01121	S57526	A53054	F64677	H36470	C69144	D37844	AI2535	JE0130	ID	
hypothetical prote	probable dna-direc	periplasmic oligop	hypothetical prote	n	coat protein - chr	hypothetical prote	hypothetical prote		hypothetical prote	hypothetical prote	probable formamido	probable membrane	isochorismate synt	phosphoribosylamid	chymosin (EC 3.4.2	ribonucleoside-dip	beta-glucosidase [nadh oxidoreductas	neuroglian - fruit	probable beta-gluc		lipoxygenase (EC 1		Wnt-7b protein - m	UDP-galactopyranos	н	hypothetical prote	scytalone dehydrat		

hypothetical protein alr7572 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet (C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004 (C;Accession: A12535
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anał A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Molecule type: DNA A;Residues: 1-605 <KUR> A;Cross-references: UNIPROT:Q8ZSD9; UNIPARC:UPI0000CCD88; GB:AP003602; PIDN:BAB77215.1;

A; Status: preliminary

45 72.5				41 73.5	-	-	-		-	35 74	34 74	33 74.5			_	
7.7	7.7	7.7	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.9	7.9	7.9	7.9	7.9	7.9	
97	430	153	4859	817	763	589	482	313	143	26926	442	667	667	436	259	
N	ب	N	N	N	N	N	N	N	N	۲	2	N	N	N	Ŋ	
A34291	LANAKO	S53544	S74173	D86217	S23457	T42244	S15748	H69984	AB1701	I38344	150110	E98339	AE2943	D70693	E69811	
pollen allergen Lo	nonstructural prot	hypothetical prote	ryanodine receptor	protein T27G7.8 [i	polysulfide reduct	probable polypepti	nitrogenase (EC 1.	conserved hypothet	hypothetical prote	titin, cardiac mus	Wnt10a protein - z	probable oxidoredu	oxidoreductase Atu	probable ugpB lipo	hypothetical prote	

ALIGNMENTS

B 8	B &	B 8	Query Ma Best Loc Matches	RESULT JE0130 scytalo C;Speci C;Acces R;Motoy Biosci A;Refer A;Acces A;Molec A;Comme C;Super C;Keywo
121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172 	61 MPAEEFVGMVSSKOMLGDPTLRTOHFIGGTRWEKVSEDEVIGYHOLRVPHORYKDTTWKE 120 	1 MGSQVQXSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60 	Query Match 98.9%; Score 932; DB 2; Length 172; Best Local Similarity 98.8%; Pred. No. 3.9e-79; Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	RESULT 1 JED0130 SCYLalone dehydratase (EC 4.2.1.94) - Pyricularia oryzae C;Species: Pyricularia oryzae C;Species: Pyricularia oryzae C;Bate: 03-Unn-1998 #sequence_revision 10-Unl-1998 #text_change 31-Dec-2004 C;Accession: JE0130 C;Accession: JE0130 R;Motoyama, T.; Imanishi, K.; Yamaguchi, I. Biosci. Biotechnol. Biochem. 62, 564-566, 1998 B;Title: cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for particular procession; JE0130 A;Accession: JE0130 A;Accession: JE0130 A;Molecule type: mRNA A;Cross-references: UNIPARC:UPI0000179D1F; DDBJ:AB004701 C;Comment: The C-terminal protein of this enzyme is important in catalysis or/and structuc;Superfamily: scytalone dehydratase C;Keywords: carbon-oxygen lyase; hydro-lyase

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A;Reference number: A69000; MUID:9803:
A;Accession: C69144
A;Status: preliminary; nucleic acid se
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:026444; UN
A;Experimental source: strain Delta H
                                                                                                                                                           R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                       UDP-galactopyranose mutase - Methanobacterium thermoautotrophicum (strain Delta C;Species: Methanobacterium thermoautotrophicum C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: C69144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Cloning and sequencing of a bile acid-inducible A;Reference number: A37844; MUID:91072253; PMID:2254270 A;Accession: D37844
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c;Species: Eubacterium sp.
c;Species: Eubacterium sp.
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 22-Oct-1999
C;Accession: D37844
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                                                                                                                                                         ki, S.; Church, G.N
J. Bacteriol. 179,
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                                                                                                                    A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463
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Best Local S
Matches 37
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 LRTQHFIGGT-RWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 DSKDWDRLRKVIAPTLRIDY------RSFLDKLWEAMPAEEFVGMVSSKQMLGDPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GVWKFAGLKPDIRWGEFDFDRIFED 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITIDSETTATGRW--YLEDRLI--
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Pred. No.
        UNIPARC: UPI0000066482;
                                                                               sequence not shown; translation
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                        GB:AE000819; GB:AE000666; NII
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A;Title: Expression of multiple novel Wnt-1/int-1-related A;Reference number: A36470; MUID:91122634; PMID:2279700 A;Accession: H36470
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                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: H36470
R; Gavin, B.J.; McMahon, J.A.;
Genes Dev. 4, 2319-2332, 1990
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C; Superfamily:
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C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
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RESULT
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Best Local &
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Best Local
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                                                                                 134 -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
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                                                                                                                                                   84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH-
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1 Similarity 22.3%;
39; Conservation
                                                                                                                                                                                 32;
                                                 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE
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                                                                                                                   QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN
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                                                                                                                                                                                                     8.9%;
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                                                                                                                                                                                     11; Mismatches
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; Pred. No. 3.4;
28; Mismatches
                                                                                                                                                                                                     Score 84; DB
Pred. No. 3.4;
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                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                          PIDN:
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO5 - Helicobacter pylori (Strain 26 C;Species: Helicobacter pylori (C;Species: Helicobacter pylori (C;Species: Helicobacter pylori (C;Bate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Dec-2004 (C;Accession: F64677 (C;Accession: F64677 (C;Accession: F64677 (C;Accession: F64677 (C;Accession: F64677 (C); Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997 (Millors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N. A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; pMID:9252185
A;Cross-references:
C;Genetics:
                                                                          A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-266 <TOM>
                                                                                                                                                        preliminary; nucleic acid
                                         UNIPROT:025852; UNIPARC:UPI00000D31A4;
                                                                                                                                                            sequence
                                                                                                                                                                not
                                                                                                                                                                shown;
                                                                                                                                                                translation
                                                 GB:AE000631;
                                                                                                                                                                    not
                                                     GB:AE000511;
                                                     NID
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A;Start codon: (C;Superfamily: 1 C;Keywords: elec

electron

NADH: quinone

oxidoreductase

idoreductase (complex I), sub membrane-associated complex;

subunit 30kD/NdhJ/NuoC
lex; NAD; oxidoreductase

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C.Species: Oryza sativa (rice)
C.Species: Oryza sativa (rice)
C.Species: Oryza sativa (rice)
C.Species: Of-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Mar-1999
C.Accession: A53054
R.Peng, Y.L., Shiźano, Y.; Ohta, H.; Hibino, T.; Tanaka, K.; Shibata, D.
J. Biol. Chem. 269, 3755-3761, 1994
A.Title: A novel lipoxygenase from rice. Primary structure and specific expression; A53054; MUID:94148883; PMID:7508918
A.;Reference number: A53054; MUID:94148883; PMID:7508918
A.;Accession: A53054
A.;Status: preliminary
A.;Molecule type: mRNA
A.;Residues: 1-923 - FENA
A.;Cross-reference; UNIPARC:UPI000017524C
A.;Experimental source: cv. Aichiasahi, blast fungus-infected leaves
A.;Note: sequence extracted from NCBI backbone (NCBIN:143808, NCBIP:143809)
A.;Note: GB:D114000; NID:9468491
C.;Superfamily: lipoxygenase
C;Keywords: oxidoreductase
                                            R;Ozcan, N.; Cunningham, C.; Harris, W.J.
submitted to the EMBL Data Library, June 1995
A;Description: Cloning of a cellulase gene fro
A;Reference number: S57526
A;Accession: S57526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <OZC>
                                                                                                                                                                                                                           cellulase - Fibrobacter succinogenes
c;Species: Fibrobacter succinogenes
C;Date: 10-Oct-1995 #sequence_revision
C;Accession: S57526
R;Ozcan, N.; Cunningham, C.; Harris, W.
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A;Cross-references: UNIPROT:Q47929; UNIPARC:UPI00000B5944; EMBL:X88561; NID:g887439; C;Superfamily: Fibrobacter succinogenes cellulase
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Species: Oryza sativa (rice)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            709 AYVARFYPDADSVAGDEELQ------AFWTEVRTKGHGDKKDAPWWPKLDSPESLAHT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 DKLW----EAMPABEFVGMVSSKQMLGDPT-----LRTQHF----IGGTRWBKV----
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Similarity 23.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VWKFAGLKPDIRWGEFDFDRIF 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SEDEVIGYHOLRVPHORYKDTTMKEVTMKGHAHSANLHWYKKIDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKLWRFDTEALPAD----LVRRGMAEEDPTAEQGLKLAIEDYPFANDGLLIWDAIKTWVQ 708
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Pred. No. 14;
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A;Cross-references: UNIPROT:048779; UNIPARC:UPI000009CB18; EMBL:AC003033; NID:g2702261; FA;Experimental source: cultivar Columbia
R;Experimental source: Cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable beta-glucosidase At2g32860 [imported] - Arabidopsis thaliana N;Alternate names: thioglucosidase homolog T21L14.20 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01121; D84738
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A;Map position: 2
A;Introns: 113/3; 137/1; 156/3; 182/1; 208/1;
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84738
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A;Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence
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                                                                                                                                                                                                 94
                                                                                                                                                                                                                                             89 GPEFEIHKQDF
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                                                                                                                                                                                                                                                                                      43 APTLRIDYRSFLDKLWEAMPAEEFVG-MVSSKQMLGDPTLRTQHFIGGTRW------E
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                                                                                                                                                                                                                                                                                                                                                                                6 QKSDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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-TFGDK 172
                                                                                                                                                        KVQQNGDGDEGVDF-
                                                                  NEEGV-KFYNDLINELLANGIQPSVTLFHWESPLALEMEYGGFLNERIVEDFREFANFCF 248
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                                                                                                              --DGVWKP-----AGLKP---
                                                                                                                                                                                                 KVSE----DEVIGYHQLRVPHQRYKD--TTMKEVTMKGHAHSANLHWYKKI------
                                                                                                                                                                                                                                                                                                                                  QPSDEDLGTIIGPHQTSFDDEIGIVIGPHATVDDEDIDMDMGTTVGPQTNLNDDDLGTII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTKVGLNDWIKVSKD----WQLAKIPLKRFTD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                            8.4%;
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23.4%; Pred. No.
                                                                                                                                                        ---YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189
                                                                                                                                                                                                                                             ·PADFIFGTSVSAYQVEG---AKKGSGRGLTSWDEFTHMFPE
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                                                                                                              ----DIRWGEFDFDRIFEDGRE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324/1; 362/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 614;
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                                                                                                                                                                                                                                                                                                                                                                              ----SKDWDRLRKVI 42
                                                                                                                                                                                                                                                                                                                                                                                                                          99;
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Praser, C.M.; Venter,
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Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylı, Rature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bieber, A.J.; Snow, P.M.; Hortsch, M.; Patel, N.H.; Jacobs, J.R.; Traquina, Z. Cell 59, 447-460, 1989
A;Title: Drosophila neuroglian: a member of the immunoglobulin superfamily with A;Reference number: A32579; MUID:90030418; PMID:2805067
A;Accession: A32579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nadh oxidoreductase I - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1239 <ENE>
A;Residues: 1-1239 <ENE>
A;Cross-references: UNIPROT:P20241; UNIPARC:UPI00001743A0; GB:M28231; NID:g157998; PIDN:
A;Note: the authors translated the codon TAT for residue 1234 as Thr and AAA for residue
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                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-265 < ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: D71838
R; Alm, R.A.; Ling, L.S.L.; Moir,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: neural cell adhesion molecule L1;
C;Keywords: alternative splicing; cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: FlyBase: FBgn0002968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: FlyBase: Nrg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroglian - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뭐
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                                                                                                                                                                                                                                             Superfamily:
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                                                                   102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWDRLRKVIA--PTL---RIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFI- 87
                        SSK---
                                                                 FYQFVG-----FSDSCKNRRRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GGTRWEKVSEDEVIGY---HQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDRPLDAPTNFTMRQIT
                                                                                                          FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV
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llarity 27.6%;
Conservative 2
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                                                                                                                                                                         8.4%; Score 79; DB 2; Length 265
21.8%; Pred. No. 7;
               -QMLGDPTLRTQHFIGG--TRWEKVSE-----DEVIGYHQ-----
                                                                                                                                                       28;
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D.; Mills, S.D.; Jiang, Q.;
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                                                                                                                                              Pred. No. /,
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.D.; Doig, P.C.; Smith Q.; Taylor, D.E.; Vovis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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orane protein
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RESULT 13
A75630
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J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Sequence Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: B96947
                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of A;Reference number: A75250; A;Accession: A75630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CAC0385
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-469 < KUR>
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                                                                           A; Note: plasmid MP1 C; Superfamily: Salmonella typhimurium ribonucleoside-diphosphate
                                                                                                                   A; Map position: m
A; Genome: plasmid
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-702 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q97M15; UNIPARC:UPI00000C9E54; A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                           A;Gene: DRB0108
                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9RZL7; UNIPARC:UPI00000D3B5A; GB:AE001826; NID:g6460827;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                       A; Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 TVKMDDKTYTKWGWEISPESLILGLEKLKEQYGDIKIYITENGLGDQ--DPIIEDEILDM
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   Similarity
32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLRIDYRSFLDKLWEAMPAEEFVGMVSSKOMLGDPTLR-TOHFIGGTRWEKVSEDEVIGY 103
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                                                                                                                                     megaplasmid
   Conservative
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19.2%; Pred. No. 14;
                     8.4%; Score 79;
25.4%; Pred. No.
                                                                                                                                                                                                                                                                                                             MUID:20036896; PMID:10567266
   21;
Pred. No. 23;
1; Mismatches
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   45;
                                         Length 702
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   28;
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                                                                                 reductase
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T.; Zalewski,
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   Gaps
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C.; Mal
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Query Match 8.2%; Score 77.5; DB 2; Length 299; Best Local Similarity 24.4%; Pred. No. 11; Matches 30; Conservative 13; Mismatches 41; Indels 39; Gaps 5;	RESULT 15 T40437 T40437 T40437 T40437 T40437 Typosphoribosylamidoimidazole-succinocarboxamide synthase - fission yeast (Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C; Accession: T40437 R; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.; Chillingworth, T.; Churcher, C.M. submitted to the EMBL Data Library, August 1999 A; Reference number: Z21929 A; Reference number: T40437 A; Residues: preliminary; translated from GB/EMBL/DDBJ A; Accession: T40437 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-299 < LYNs A; Residues: 1-299 < LYNs A; Residues: 1-299 < LYNs A; Residues: UNIPROT: Q9UUB4; UNIPARC: UPI0000132AAE; EMBL: AL109822; PIDN: CAB52612. C; Genetics: C; Genetics: A; Gene: SpDB: SPBC409.10 A; Map position: 2 C; Superfamily: phosphoribosylaminoimidazolesuccinocarboxamide synthase	Qy 3 SQVQKSDEITFSDYLGLMTCVY-EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWE 59	RESULT 14 147176 chymosin (EC 3.4.23.4) precursor - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Oct-2004 C;Accession: 147176 R;Foltmann, B.; Jensen, A.L.; Loenblad, P.; Smidt, E.; Axelsen, N.H. Comp. Biochem. Physiol. A 68, 9-13, 1991 R;Tile: A Developmental Analysis of the Production of Chymosin and Pepsin in Pigs. A;Reference number: 147176 A;Reference number: 147176 A;Residue: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-380 <fol> A;Cross-references: UNIPROT:Q28950; UNIPARC:UPI0000088E4A; EMBL:U14406; NID:g540096; PID C;Superfamily: Pepsin C;Keywords: aspartic proteinase; hydrolase Query Match Best Local Similarity 24.6%; Pred. No. 12; Matches 43; Conservative 21; Mismatches 62; Indels 49; Gaps 8;</fol>	Qy 58 WEAMPABEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRV 108
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Search completed: December 5, 2006, 01:28:09 Job time : 42 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications AA New:*

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

esult No.	Score	Query Match	Query Match Length	₽B	ID	Description
ב	942	100.0	172	6 !	US-10-507-132-2	Sequence 2, Appli
N	938	99.6	172	σ	US-10-507-132-4	Sequence 4, Appli
w	87	9.2	941	σ	US-10-449-902-44748	44
4.	80.5	8.5	444	7	US-11-174-307B-3704	3704,
ហ	79.5	8.4	614	7	US-11-056-355B-70678	
თ	79.5	8.4	615	7	US-11-056-355B-78750	78750,
7	77	8.2	375	7	US-11-056-355B-65439	65439,
80	77	8.2	436	თ	US-10-449-902-30829	30829,
9	77	8.2	436	0	US-10-449-902-50460	50460,
10	77	8.2	844	σ	US-10-449-902-52228	52228,
11	76.5	8.1	596	σ	US-10-449-902-47097	47097,
12	76.5	8.1	827	σ	US-10-449-902-41550	41550,
13	76	8.1	537	9	US-10-953-349-24962	
14	76	8.1	634	σ	US-10-953-349-24961	24961,
15	76	8.1	664	6	US-10-953-349-24960	24960,
16	75.5	8.0	430	7	US-11-293-697-4232	4232,
17	75	8.0	497	7	US-11-282-262-9	Sequence 9, Appli
18	74.5	7.9	359	σ	US-10-953-349-22948	
19	74.5	7.9	393	σ	US-10-953-349-22947	Sequence 22947, A
20	73.5	7.8	564	7	US-11-056-355B-76449	76449,
21	73.5	7.8	615	7	US-11-056-355B-76448	
22	73.5	7.8	763	7	-11	8316,
23	73.5	7.8	809	7	US-11-056-355B-76447	
24	73	7.7	319	σ	-10	5612,
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72 7.6 215 6 US-10-805-394-5489 72 7.6 546 7 US-11-056-3558-7080 72 7.6 547 7 US-11-056-3558-70879 72 7.6 548 7 US-11-056-3558-70879 72 7.6 548 7 US-11-056-3558-70879 72 7.6 549 7 US-11-056-3558-70879 72 7.6 973 7 US-11-056-3558-70879 71.5 7.6 651 6 US-10-511-937-2401 71.5 7.6 651 7 US-11-329-941-2 71.7 7.5 565 7 US-11-329-941-2 71.7 7.5 1169 6 US-10-449-902-41184 70.7 7.5 818 6 US-10-449-902-51784 70.7 7.4 239 7 US-11-056-3558-19951 70 7.4 327 7 US-11-056-3558-19950 70 7.4 391 7 US-11-056-3558-19950 70 7.4 391 7 US-11-056-3558-19950 70 7.4 391 7 US-11-056-3558-19949 70 7.4 785 6 US-10-449-902-47774 70 7.4 785 6 US-10-449-902-36376	45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	ω	30	29	28	27	į
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03-10-805-394-5489 03-11-056-355B-78680 03-11-056-355B-78679 03-11-056-355B-78751 03-11-056-355B-78751 03-11-056-355B-78751 03-11-30-403-9960 04-10-511-937-2401 03-11-357-421-206 04-10-449-902-41184 03-10-449-902-41184 03-10-449-902-51784 03-10-449-902-51784 03-10-449-902-51784 03-10-449-902-36376 03-10-449-902-36376 03-10-449-902-36376 03-10-449-902-36376 03-10-449-902-36376	785	785	415	391	327	325	239	818	1254	1169	565	651	651	973	549	548	547	546	215	1 1
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	US-10-449-902-52542	US-10-449-902-47774	US-10-449-902-36376	US-11-056-355B-19949	US-11-056-355B-19950	US-10-449-902-50076	US-11-056-355B-19951	US-10-449-902-51784	US-11-366-965-1028	US-10-449-902-41184		US-11-329-941-2	US-10-511-937-2401	US-11-330-403-9960	US-11-056-355B-78751	-11	US-11-056-355B-78752	US-11-056-355B-70680	US-10-805-394-5489	11 444 1144
	52542, A	47774, A	36376, A	19949, A	19950, A	50076, A	19951, A	51784, A	1028, Ap	41184, A	206, App	2, Appli	2401, Ap	9960, Ap	78751, A	70679, A	78752, A	70680, A	5489, Ap	10000

ALIGNMENTS

RESULT 1

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RESULT 4
US-11-174-307B-3704
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LENGTH: 172
TYPE: PRT
Sequence 3704, Application
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44748
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Best Local Similarity
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Publication No. US20060123505A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: FULL-LENGTH PLANT CDNA FILE REFERENCE: MOA-A0205Y1-US CURRENT APPLICATION NUMBER: US/10/449,902 CURRENT FILING DATE: 2003-05-29 PRIOR APPLICATION NUMBER: JP 2002-203269 PRIOR PILING DATE: 2002-05-30 PRIOR PILING DATE: 2002-12-11 PRIOR FILING DATE: 2002-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2004-09
PRIOR APPLICATION NUMBER: JP:
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 56791
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Local Similarity 23.0%;
hes 34; Conservative 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                                                                             VQAYVARFYPDADSVAGDEELQ-----AFWTEVRTKGHGDKKDAPWWPKLDSPESLA 776
                                                                                                                                                                                             -----SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG-----
                                                                                                                                                                                                                                DKLWRFDMEALPAD----LVRRGMAEEDPT--AEHGLRLAIEDYPFANDGLLIWDAIKTW 724
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16; Mismatches
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND
TITLE OF INVENTION: USEFUL FOR MODIFYING PLA
FILE REFERENCE: 2750-1601PUS2
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION:
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PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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INFORMATION:
INFORMATION:
265
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                                                                                                                                                      159 LAKERES--AEAYLGRAIQEAIVTVPQQYNDP------
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                                      EFDFDRIFED-----GRETFGDK 172
                                                                                                                  V-----PHQRYKDT-TMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWG
                                                                                                                                                                                               LDKLWEAMPAEEFVG-----MVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLR
GQDFDQRIVDHFVELIRKKHGKDLSNDK
                                                                           MIDEPTAAAVAHGLHRKLRDEGNVLVLHVGGGTSDASVMWY--VDGVFEFMGADEDPFFG
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                              GI Number: 2642238; NR Description: endoplasmic reticulum HSC70-cognate binding protein precursor [Glycine max] sgi|11277127|pir||T46574 dnaK-type molecular chaperone Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI Number: 19811; NR Description: luminal binding protein (BiP) [Nicotiana tabacum] -gi|100339|pix||S21879 dnaK-type molecular chaperone blp4 precursor - common tobacco -gi|729620|sp|003684|BIP4_TOBAC Luminal binding homolog 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI Number: 19813; NR Description: luminal binding protein (BiP) [Nicotiana tabacum] sgi|100340|pir||S21880 dnaK-type molecular chaperone blp5 precursor - common tobacco sgi|729623|sp|Q03685|BIP5_TOBAC Luminal binding homolog 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI Number: 13398537; NR Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI Number:
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23.6%;
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(BiP) (78
                                                                                                                                                                                                                                  Score 80.5; DB Pred. No. 6.7; S; Mismatches
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                                                                                                                                                                                                                                                                       Length 444;
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US-11-056-355B-78750
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PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 70678
LENGTH: 614
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                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 78750
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                                                                                                                                                                                                                                        TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14
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APPLICANT: Alexandrov, Nickolai
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LOCATION: (1) (614)
OTHER INFORMATION: Ceres Seq.
                 NAME/KEY: peptide
LOCATION: (1)..(615)
OTHER INFORMATION: Ceres
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ORGANISM: Arabidopsis thaliana
                                                                                               TYPE: prt
ORGANISM: Arabidopsis
                                                                              FEATURE:
                                                                                                                                        LENGTH: 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 --DGVWKF-----AGLKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 KVQQNGDGDEGVDF-----YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
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23.2%; Pro
vative 29;
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                 Seq. ID no.
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Pred. No. 1:
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WESULT 8
US-10-49-902-30829
; Sequence 30829, Application US/10449902
; Publication No. US20060123505A1
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US-11-056-355B-65439
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Best Local S
Matches 57
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LENGTH: 375
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERENCE: 2750-1590PUS2
CURRENT APPLICATION UNMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-02-13
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LOCATION: (1)..(3
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                                                                                                                                                                                                                                                                174 KWADGKKFED-----KFVDTLLKYGYRGQYMSENWLKQPLFIQSFAPSSLVHVSNLTDSP
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57; Conser
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                                                                                                                                                 TMKGHAHSANLHWYK-KIDGVWKFAGLKPDIRWGEFDF-----DRIFED 164
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                                                                                                              VARAHAHNLOVHPYTYRNENQFLHFDFHQD-PYAEFDFWINTMGVDGLFTD 337
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23.2%; Pred. No. 12;
tive 29; Mismatches
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Pred. No. 1
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12;
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GENERAL INFORMATION:

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RESULT 10
US-10-449-902-52228
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US-10-449-902-50460
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50460
LENGTH: 436
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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PRIOR APPLICATION NUMBER: JP 2002-383870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 2002-203269
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                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 KNLDFLKTVMDRLPGVRIAFIGDGPYRSELEKMFEGMPA-VFTGMMQGEEL------SQ 294
                                                                                          295 AYASGDVFVMPSESETLG 312
                                                                                                                                      85 HFIGGTRWEKVSEDEVIG 102
                                                                                                                                                                                                                                33 KDWDRLRKVI--APTLRI-----DYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 HFIGGTRWEKVSEDEVIG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 KDWDRLRKVI--APTIRI-----DYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                    KNLDFLKTVMDRLPGVRIAFIGDGPYRSELEKMFEGMPA-VFTGMMQGEEL------SQ 294
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32.1%; Pred. No.
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32.1%; Pred. No.
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14;
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US-10-449-902-52228
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US-10-449-902-47097
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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-002051-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-39

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR APPLICATION NUMBER: JP 2002-383870

PRIOR APPLICATION NUMBER: JP 2002-383870
                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47097
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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH FLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

CURRENT FILING DATE: 2003-05-29
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SEQ ID NO 52228
LENGTH: 844
                                                                                                     Matches
                                                                                                                       Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR TILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
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                                                                                                                                                                                                                                                       PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
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                                                 26 WADSY--DSKDWDRLRKVIAPTLRIDYRSFLDKLWE-----AMPAEEFVGMVSSKQM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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WGHSVSGDLLNWAALDTALDPTSPFD----ANGCWSGSATILPGALPAILYTGIDASKEO 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YHWLCSPNPDFNEI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MNWYKG----WK--GLFP 696
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                                                                                                     Conservative
                                                                                                8.1%; Score 76.5; I
22.5%; Pred. No. 23;
ative 21; Mismatches
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                                                                                                                                                 DB 6;
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                                                                                                                                               Length 596;
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RESULT 13
US-10-953-349-24962
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US-10-449-902-41550
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SOFTWARE: Patentin version 3.3
SEQ ID NO 24962
LENGTH: 537
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Publication No. US20060107345A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41550
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Best Local Similarity 27.8%;
                                                                                        Matches
                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
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                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                               / Match 8.1%;
Local Similarity 20.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 AHSANLHWYKKIDGVWKFA-----GLKPDIRWGEFDFDR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                         56 KLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR-----
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                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 QVQKSD-----EITFSDYLGLMTCVYE-----
KLWRFDMESLPAD----LIRRGMAVDDPSMPC----GVKLVIDDYPYAADGLLIWSAIK 319
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                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                        2004-09-30
                                                                                          23;
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Pred. No. 35;
9; Mismatches
                                                                                                             Score 76; DB
Pred. No. 23;
                                                                                        Pred. No. 23;
3; Mismatches
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                                                                                                                                    DB 6;
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                                                                                        43; Indels
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                                                                                                                                  Length 537;
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                                         -----WEKVS 96
                                                                                      Gaps
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CURRENT APPLICATION NUMBER: US/10/953,349;
CURRENT FILING DATE: 2004-09-30;
NUMBER OF SEQ ID NOS: 40252;
SOFTWARE: PatentIn version 3.3;
SEQ ID NO 24961;
LENGTH: 634;
TYPE: PRT;
ORGANISM: Glycine max
US-10-953-349-24961
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US-10-953-349-24961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24960
LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24961, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24960, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                Matches
                                                                                                   Query Match
Best Local :
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Best Local (
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                     TYPE: PRT
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 KLWRFDMESLPAD----LIRRGMAVDDPSMPC-----GVKLVIDDYPYAADGLLIWSAIK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 IWIASGQHAAINFGQYPF 397
  396 KLWRFDMESLPAD----LIRRGMAVDDPSMPC----GVKLVIDDYPYAADGLLIWSAIK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 VWKFAGLKPDIRWGEFDF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 EWVESYVAHFYSDPNSVTSDVELQAWWREIKLKGHSDKKNEPWWPKLDTKEDLSGILTTM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 VWKFAGLKPDIRWGEFDF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 E-DEVIGYHOLRVPHORYKDTTM----KEVTMKGHAHSANLHWYKKIDG------
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                                      56 KLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR-----WEKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EWVESYVAHFYSDPNSVTSDVELQAWWREIKLKGHSDKKNEPWWPKLDTKEDLSGILTTM 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.1%; Score 76; DB 6; 20.3%; Pred. No. 28;
                                                                                               8.1%; Score 76; DB
20.3%; Pred. No. 30;
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                                                                            Mismatches
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                                                                                                                    6; Length 664;
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                                                                              Indels
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                                                                              7;
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OM protein protein search, using sw model GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title: Perfect score: December 5, 2006, 01:39:46; Search time 187 Seconds (without alignments)
426.059 Million cell updates/sec

Run on:

Scoring table: Sequence: BLOSUM62 US-10-507-132-2 942 1 MGSQVQKSDEITFSDYLGLM......WGEFDFDRIFEDGRETFGDK 172

Searched: 2097797 seqs, 463214858 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No.	Score	Query Match	Length	DB B	ID	Description
1	87		924	σį	US-10-491-733-22	
N	85	9.0	265	ω	-09-882-227	טע סע
ω	84	•	349	ຫ	-10-847-972-6) (
4	84	8.9	349	o	-11-108-506	100
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ه د	9 4) <u>+</u>		-10-425-115-	213
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, ,	81	ó	349	4	-10-364-88	ω i
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1 1	20 00	. 6	349	0	Ļ	(D
, ,t	٠		614	6	US-11-096-568A-28399	e 2839
. J.			1239	6	US-11-097-143-1701	e 1701.
jσ			266	4	35-977-642	6427
	20 /9		702	4.	-234	
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2 4		٠	424	4	US-10-424-599-282063	e 282067
, C	2 6	٠	861	σ	7-099-	1420.
) N			861	σ	8-123	12347
2 6			2195	4.	-10-437-	181567
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) A		•	869	4	US-10-437-963-142051	14209
2 0	1 .	٠	375	σ	-11-096-568	13512
) () (7,	ο α	436	4.	-10-437-963-	Sequence 178354,
!	;		044	4	US-10-437-963-132118	13211

RESULT 2
US-09-882-227-306
US-09-882-227-306
Sequence 306, Application US/09882227
Publication No. US20030158396A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean-Francois

4.5	44	. <u>.</u>		45	41	40) (a	ינ	7	36	3.5) (ى ر د	יי	32	31		20	29		28
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US-09-996-634-136	US-10-282-122A-64780	US-10-282-122A-62311	US-10-437-963-136067	OC 10-109-193-2415	IIS-10-360-403-2412	US-10-696-616-20	US-11-188-298-12759	US-10-179-766-9	US-10-437-963-154890			US-10-369-493-1784	US-10-108-260A-4232	US-10-U32-585-7157	10 10 000 and and	US-10-955-745-79	US-10-289-757-79	05-10-4/3-193-51	10 10 111 100 01	US-10-314-657-51	US-10-481-032A-70	
Sequence 136, App		_	Sequence 136067,	sequence 2413, Ap					Sequence 154890,	sequence 155, App	1 0		423	Sequence 7157, Ap	Tddw 'A' Abbr	3 .	70	Seguence 51. Appl	rddw 're annanhae		Sequence 70 Anni	

ALIGNMENTS

B &	? 분	δ	B 8	Query M Best Lo Matches	RESULT 1 US-10-49 IUS-10-49 IUS-10-4
760 HTLTTIVWVAAAHHAAVNEGQYDEGGYF 787		96SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG 140	55 DKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKV 95 : : : : : :	Query Match 9.2%; Score 87; DB 5; Length 924; Best Local Similarity 23.0%; Pred. No. 8; Matches 34; Conservative 16; Mismatches 44; Indels: 54; Gaps 7;	RESULT 1 US-10-491-733-22 ; Sequence 22, Application US/10491733 ; Publication No. US20040219675A1 GENERAL INFORMATION: APPLICANT: Syngenta Participations AG APPLICANT: Salmeron, John APPLICANT: Salmeron, John APPLICANT: Weislo, Laura J. TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic St. TITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality and CURRENT FILLING DATE: 2004-04-05 ; PILE REFERENCE: 60127WOPCT ; CURRENT FAPPLICATION NUMBER: US/10/491,733 ; CURRENT FILING DATE: 2004-04-05 ; PRIOR APPLICATION NUMBER: 60/334,501 ; PRIOR FILING DATE: 2001-11-30 ; NUMBER OF SEQ ID NOS: 64 ; SSOFTWARE: PatentIn version 3.1 ; SEQ ID NO 22 ; LENGTH: 924 ; TYPE: PRT ; ORGANISM: Oryza sativa

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 306
LENGTH: 265
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60, Application US/10847972

Publication No. US20050049195A1

GENERAL INFORMATION:
APPLICANT: ZOU, YIMIN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
FILE REFERENCE: ARCD:395US
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                                                                                                                                                                    Query Match
Best Local S
Matches 32
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Best Local 9
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CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
                                                                                                                                                                                                                                                                                                              SEQ ID NO 60
LENGTH: 349
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TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/847,972
CURRENT FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/470,913
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: VARIANT
LOCATION: 118
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 39; Conserv
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131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
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                                                                                  74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN
                                                                                                                          84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS------ANLH- 133
                                                                                                                                                                  h 8.9%; Score 84; DB 5; Length 349;
Similarity 31.1%; Pred. No. 4.8; .
32; Conservative 11; Mismatches 36; Indels
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                                            -WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
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RESULT 4 US-11-108-528-46

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TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CEI
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: HYDR-P01-041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR FILING DATE: 2004-08-08
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
PRIOR FILING DATE: 2004-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         SEQ ID NO 56305
LENGTH: 411
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APPLICANT:
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                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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TYPE: PRT
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                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: UC-ZMFLB73131C10_FLI.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRFVDARE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 -----WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                    171 WKDVFDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 OHOFREGRWINCSALGEKTVEG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                         26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF-----LDK-----LW-EAMPAEEFVGMV 70
71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
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                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Elizabeth
Chen, C. M. Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marvin, Martha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Dean Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%;
                                                                                                                                       8.9%;
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                                                                                                                    17; Mismatches
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Pred. No. 4.8;
                                                                                                                                       Score 84; D
Pred. No. 5.
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                                                                                                                                         DB 4; Length 411;
5.9;
                                                                                                                         31; Indels
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US-10-285-976-21
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; OTHER INFORMATION: Clone ID: MRT4577_126150C.1.pep
US-10-425-115-213325
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US-10-425-115-213325
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               SOFTWARE: PatentIn Ver. SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Appropriation No.
                                                                                                                                                                                                                                                         APPLICANT: Rhee,
APPLICANT: Walin:
APPLICANT: Wu. CI
APPLICANT: Leoni
APPLICANT: Carro,
APPLICANT: Carro,
APPLICANT: The Ro
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Best Local Similarity
                                           APPLICANT: Carson, Dennis A.

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wht and Frizzled Receptors as Targets for 1
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
TILE REFERENCE: 0.23070-130320US
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2001-05-01
PRIOR PILING DATE: 2001-05-01
PRIOR PILING DATE: 2002-05-01
NUMBER: WO PCT/US02/13802
NUMBER: OF SEQ ID NOS: 232
SOFTWARER: DEFERIT VOT: 2
SOFTWARER: DEFERIT VOT: 2
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LENGTH: 411
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF-----LDK----LW-EAMPAEEFVGWV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKDVFDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TEVDFF---SKWQQVL----YHWLCSPNPDFNEI----
                                                                                                                                                                                                                                                                                                Leoni, Lorenzo
Corr, Maripat
                                                                                                                                                                                                                                                                                                                                         Wu, Christina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MNWYKG----WK--GLFP 268
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                                                                                                                                                                                                                                                                                                                   Lorenzo M.
                                                                                                                                                                                                                                                                                                                                                              Sen
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25.2%;
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Pred. No.
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                                                                                                                                                                                                                             Targets for Immunotherapy
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US-10-364-888-2
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APPLICANT: Rastelli,
APPLICANT: Zhong, Ha
APPLICANT: Boldog, F
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 2
                                                                                                                                     Matches
                                                                                                                                                                Query Match
                                                                                                                                                      Best
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APPLICANT:
APPLICANT:
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APPLICANT: Edinger, Shlomit
APPLICANT: Edinger, Shlomit
APPLICANT: Burges, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
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                                                                                                                                                                                                             LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                    Local
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138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                               134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                 Similarity
                                                            RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137
                                                                                             RW--EKVSEDEVIGYHOLRVPHORYKDTTMKEVTMKGHAHS-----ANLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 31.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets, Richard
Spytek, Kimberly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guo, Xiaojia
Malyankar, Uriel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vernet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pena, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gangolli, Esha
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Boldog, Ferenc
                                                                                                                                   Conservative
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                                                                                                                                                 8.6%;
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                                                                                                                              11;
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                                                                                                                                                 Score 81; DB
Pred. No. 10;
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Pred. No.
                                                                                                                              Mismatches
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                                                                                                                               31;
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                                                                                                                                                             Length 349;
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US-10-364-888-6

Sequence 6, Application US/10364888 Publication No. US20040023259A1

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FILE REFERENCE: 1596-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR RILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOPTWARE: CuraSeqList version 0.1
SEQ ID NO 6
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APPLICANT: Rastelli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, App
Publication No.
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APPLICANT:
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APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                           APPLICANT:
                              APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rastelli, Luca APPLICANT: Zhong, Haihon
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: 60/387,082 FILING DATE: 2002-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
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                                                                                                                                                                                                                                                                                                                                                                       Zhong, Haihong
Boldog, Ferenc
Gangolli, Esha
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Malyankar, Uriel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gangolli,
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Pena, Carol
                                                                                                                                                                                                                                                                                                                                       Malyankar, Uriel
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Rieger, Daniel
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                                                                                                                                                                                                                                                                          Richard
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; Pred. No. 10;
11; Mismatches
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US-10-847-972-22

Sequence 22, Application US/10847972
Publication No. US20050049195A1
GENERAL INFORMATION:
APPLICANT: 20U, YIMIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION

RESULT 12

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                                                                                                                                                                                                                                            ; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wingless-type 7B (Wnt-7B) peptide sequence
US-10-678-639-20
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CURRENT APPLICATION NUMBER: US/10/678,639
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: US 10/264,825
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US 60/509,037
PRIOR FILING DATE: 2002-10-04
PRIOR FILING DATE: 2002-10-04
PRIOR PPLICATION NUMBER: US 60/491,350
PRIOR PPLICATION NUMBER: US 60/491,350
PRIOR FILING DATE: 2003-07-31
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LENGTH: 349
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Best Local
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Best Local S
Matches 30
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PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: He, Biao
APPLICANT: You, Lie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jablons, David M.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 34
TYPE: PRT
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                                        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
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                                                                                                                                                               h 8.6%; Score 81; DB Similarity 31.2%; Pred. No. 10; 30; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Ver.
QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                                                                         RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-----ANLH-----
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Xu, Zhidong
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Pred. No. 10;
                                                                                                                                                                                                            5; Length 349
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                                                                  US-11-096-568A-28399
                                                                                  RESULT 14
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SEQ ID NO 22
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/847,972
CURRENT FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/470,913
PRIOR FILING DATE: 2003-05-15
           Sequence 28399, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 44
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                                                                                                                                                                                                                                                                                                                       Query Match
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PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Marvin, Mart
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CURRENT FILING DATE: 2005-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: HYDR-P01-041
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                         QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/11108528
No. US20050261189A1
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Chen, C. M. Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marvin, Martha
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31.2%; Pred. No. 10;
ative 11; Mismatches
Nickolai et al
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Pred. No.
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                                                                                                                                      PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILLING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
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Publication No. US20050208558A1
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Best Local S
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FILE REFERENCE: 2750-15920US2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
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NAME/KEY: misc_feature
LOCATION: (1)...(614)
CONTROL TRECORMATION: CEY
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1701
                                                             PRIOR APPLICATION NUMBER: 60/184,831 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: 60/191,637 PRIOR FILING DATE: 2000-03-23
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OTHER INFORMATION:
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE:
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57; Conserv
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                         FastSEQ for Windows Version
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Pred. No. 29;
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Result
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Maximum DB seq length: 200000000
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-Q=Abss/ABsSWEB spool/(S10507132/runat 04122006 143903 11302/app query.fasta 1
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000 -HOST=abss07
-USER-US10507132 @CCN1 1 16323 @runat 04122006 143903 11302 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Perfect score:
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                                                                                             Score
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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Match
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942
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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BM864194 mgcm008xJ
BM863315 mgcm006xE
BM863340 mgcm006xK
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ALIGNMENTS

	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 BM863356
Contact: Ebbole DJ Contact: Ebbole DJ Contact: C	grisea Unpublished (2002) On Mar 7, 2002 this sequence version replaced gi:19231038.	Bhatterai, K. and Dean, R.A. Expressed sequence tags from the rice blast fungus, Magnaporthe	<pre>1 (bases 1 to 619) Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,</pre>	 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 	Magnaporthe grisea	Magnaporthe grisea (anamorph: Pyricularia grisea)	EST.	BM863356.2 GI:30391591	<pre>grisea cDNA clone mgcm006x003 5', mRNA sequence. BM863356</pre>	Libr	

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Best Local Similarity:
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                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                           41 VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
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                                                                                                                                                                                                                      IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
                                                                                                                                    ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTTpTyrLysLysIleAspGly
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IlePheGluAspGlyArgGluThrPheGlyAspLys 172
                                                               ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg
                                                                                                                                                                                       ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                                                                                                                                                                                                                                    CTCCGCACGCAGCATCATCGGCGGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTC
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/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptsK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h. room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredbrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/clone="mgcm006x003"
/sex="Mat1-2 hermaphrodite"
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US-10-507-132-2 (1-172) x BM864194 (1-657)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
On Mar 7, 2002 this
Contact: Ebbole DJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson Bldg, MS2132, College
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Pathology & Microbiology
Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: T3 primer BACKWARD: T7 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbole@tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 657)
                                                                                                                                                                                                                            /Clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
//clone="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="mgcm008xJ12"
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MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet

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                                                                                                                                                                                                  On Mar 7, 2002 this sequence version reprint the Contact: Ebbole DJ
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132,
Tel: 979 845 4831
Fax: 979 845 4833
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mgcm006xE21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xE21 5', mRNA sequence.
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                                                                                                       PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
                                                                                                                                           Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...364 e-100
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1 (bases 1 to 664)
                                                                                        Plate: mgcm006 row:
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                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM863315.2 GI:30391622
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                                                                       primer: T3.
         organism="Magnaporthe grisea"
/mol_type="mRNA"
                                            1. .664
/strain="Guy11"
                                                          Location/Qualifiers
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RESULT 4 BM863340 LOCUS

DEFINITION

mgcm006xK09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xK09 5', mRNA sequence.
BM863340
BM863340.2 GI:30391603
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Query Match:
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                            VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
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ATCTTTGAGGACGGACGGGAGACCTTGGGCGACAAA 596
                                                                                       GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG
                                                                                                                 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
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/clone="mgcm006xE21"
/sex="Mat1-2 hermaphrodite"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                      144
      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromatogram file of this sequence is available, see contact person; Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peterson Bldg, MS2132, College Station, TX 77843-2132, Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: d-ebbole@tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
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                                                                          VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
                                                                                                                                    ACTTGCGTCTATGAGTGGGCAGACAGCTACTACTCCAAGGACTGGGATAGGCTGCGAAAG
                                                                                                                                                                                                                                                MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet
                                                                                                                                                                                                                            ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
                                                                                                                                                                    ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKWAKD: T7 primer
te: mgcm006 row:
primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
//clone | lib="Magnaporthe grisea CM Uni-Zap XR Library"
//note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
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/clone="mgcm006xK09"
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923.00
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                                                                                                                                                                                                                                                                                                                                                                                                         Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|. . . 322 2e-87
PCR. PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas A&M University
Peterson Bldg, MS2132, College
Tel: 979 845 4831
Fax: 979 845 6483
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On Mar 7, 2002 this
Contact: Ebbole DJ
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                                                                                                                                                                                                                                                                                                                                                    Plate: mgcm006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Pathology & Microbiology
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                                                                                                                                                                                                                                                                                                                            primer: T3.
              /cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone="Vector: pBluescriptSK-; Site_1: EccRI; Site_2:
XhoI; Unidirectional cloning. EccRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
                                                                                                                                                                                                     /organism="Magnaporthe grisea"
/mol_type="mmxA"
/strain="duy11"
/db_xref="taxon:148305"
reinoculated into complete
                                                                                                                                                               /clone="mgcm006xF04"
/sex="Mat1-2 hermaphrodite"
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Best Local Similarity:
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                                                                                                                                                                                                                                           mgcm007xE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm007xE24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μ
Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19231392.
                                                                           Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (Dases 1 to 571)
Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
                                                                                                                                                                       Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                        Expressed sequence tags from
                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                             BM863710.2
                                                                                                                                                                                                                                                                                                                                                                                                   ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys
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                                                                                                                                                                                                                                                                                                                                                                             ATCTTTGAGGGCGGACGGGAGACCTTTGGCGACAAA
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Matches:
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Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbol@Gramu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
gerson;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91
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Tel: 979 845 4831
Fax: 979 845 6483
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BACKWARD: T7
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                                                                                                    LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
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                    IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
                                                                                                                                                                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/mol_type="mRNA"
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/sex="Mat1-2 hermaphrodite"
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RESULT 7
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                                           Best Local Similarity:
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                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm008 row: I
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77
Tel: 979 845 4831
Fax: 979 845 6483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp[P56221] SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence tags from the grisea
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Magnaporthe grisea
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1 (bases 1 to 599)
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                                                                                                                                                                        /cell type="mycellum"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wettor: pBluescriptsK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredbrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:148305"
/clone="mgcm008xD02"
/sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Guy11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Magnaporthe grisea"
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                                                                          Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see conta
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR
dehydratase >gi|1127197|pdb|1STD|...320 8e-87
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Tel: 979 845 4831
Fax: 979 845 6483
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Contact: Ebbole DJ
Department of Plant Pathology
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//sex="Mat1-2 hermaphredite"
/cell_type="mycelium"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone lib="Magnaporthe grisea CM Iside has T3 primer and predominantly 5 reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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                                                                             Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel: 979 845 4831

Fax: 979 845 6483

Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|...308 3e-83
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Contact: Ebbole DJ
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Bhatterai,K. and Dean,R.A.
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                          ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
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                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="mycellum"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
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XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/clone="mgcm005xD02"
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Matches:
Conservative:
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SOURCE
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BM863558
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                                                                                                                                                                                                                                                        BACKWARD: T7 primer
Plate: mgcmnoc
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ
Department of Plant Pathology & Microbiology Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77 Tel: 979 845 4831
Pax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mgcm006xH04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xH04 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                   Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp[P56221]SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...272 3e-72
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Magnaporthe grisea
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FORWARD: T3
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EST.
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te: mgcm006 row:
primer: T3.
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/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library" /note="Vector: pBluescriptSK; Site 1: EcoRI, Site 2: XhoI; Unidirectional cloning. EcoRI side has T3 prImer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended,
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/mol_type="mRNA"
/strain="Guy11"
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                                                                                                                                 clone="mgcm006xH04"
                                                                                                                                              db_xref="taxon:148305"
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reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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Percent Similarity:
Best Local Similarity
Query Match:
DB: Alignment Pred. No.: US-10-507-132-2 (1-172) Score: No.: 573 160 514 141 455 121 395 101 335 275 215 155 Similarity: 81 61 41 21 95 gIlePheGluAspGlyArgGluThr 168 -ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspAr GTCACCATGAA-GGGCCACGCCCACTCGGCAAACCTTTACTTGTACAAGAAGATCGACGGC IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys GGTTCTTTAGGACGGACGGGAAACC GGCTTGGAGGTTCGCGGGCCTAAACCCCCGACTT-CGGTGGGGCGAGTTCCAATTTTACAG ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAA CTCCGCACGCACTTCATCGCCGCGCACGCGCTGNGAGAAGGTGTCCGAGGACGAGGTC 1.66e-84 772.00 93.5% 91.1% 82.0% × BM863558 (1-602)Length: Matches: Conservative: Mismatches: Indels: Gaps: 597 154 154 10 10

120

454 140

513

160 572 100

394

334

60 274 80 154

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RESULT 11 BM863639 LOCUS VERSION KEYWORDS DEFINITION REFERENCE SOURCE ACCESSION TITLE ORGANISM 486 bp mRNA linear EST mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library grisea cDNA clone mgcm007xG13 5', mRNA sequence.
BM863639 grisea Ebbole, D.J., Yuan, J., Thomas, T.L., Bhatterai, K. and Dean, R.A. Magnaporthe grisea EST Expressed sequence Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe Eukaryota; Fungi; Ascomycota; Unpublished Magnaporthe BM863639.2 (bases 1 to 486) GI:30391353 grisea (anamorph: (2002)tags from the Pezizomycotina; Pyricularia rice Bobrowicz, P., blast fungus, Magnaporthe grisea) Sordariomycetes; Lu, G. 06-MAY-2003 Magnaporthe

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PCR PRimers
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Tel: 979 845 4831
Fax: 979 845 6483
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Contact: Ebbole
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                 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu
                                                                                               LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
                                                                                                                                                   ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
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ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                                       CTCCGCACGCACTTCATCGGCGCACGCGCGCGGGAGAAGGTGTCCGAGGACGAGGTC
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/Celne lib="Magnaporthe grisea CM Uni-Zap XR Library"
/Colone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
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Strain inoculated into complete medium grown for two days
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according to phd files (0.05) and for vector seqs."
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Query Match:
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Seq primer: T3.
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Fax: 979 845 6483
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Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Assomycota; Pezizomycotina; Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp[P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...271 le-71
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/Cell_type="Appressorium"
/Celone lib="Magnaporthe grisea Ap Uni-Zap XR Library"
/clone lib="Magnaporthe grisea Ap Uni-Zap XR Library"
/note="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Appressorium library. Conidia were germ inated on an inductive surface for 5-8 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector
                                                                                                                                                                                                                                                                                                                         /clone="mgap007xA05"
/sex="Mat1-2 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:148305"
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/strain="70-15"
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FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row:
Seq primer: T3.
                                                                                                                               Unpublished (2002)
On Mar 7, 2002 this sequence version replaced gi:19231
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132,
Tel: 979 845 483
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510 bp mRNA linear EST 06-MAY-2003 mgcm006xC10f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xC10 5', mRNA sequence.
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Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                      Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|I127197|pdb|ISTD|... 276 le-73
PCR. PRimers
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Magnaporthe grisea (anamorph: Magnaporthe grisea Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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mgcm006x005f.b Magnaporthe grisea CM Uni-Zap XR Library grisea cDNA clone mgcm006x005 5', mRNA sequence.
BM863357
BM863357.1 GI:19231039
EST.
                                                                                                                                                                                                                                                                                                                    GTCACCATGAAGGGCCACGCTCACTCGGCAAACCTT
                                                                                                                                                                                                                                                                                                                                                   ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
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/sex="Mat1-2 hermaphrodite"
/sex="Mat1-2 hermaphrodite"
/cell type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_7:
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_1: XhoI, Unidirectional cloning. EcoRI side has T3 primer and predominantly 5', reads. T7 primer on XhoI side of insert.
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Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD| . . . 276 le-73
PCR PRimers
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Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: mgcm006
Seq primer: T3.
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LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
                                                                               MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 prImer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/clone="mgcm006x005"
/clone="mathin"
/sex="Mathin"
/cell_type="my/cellium"
/clone_lib="Magnaporthe gri
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On Mar 7, 2002 this
Contact: Ebbole DJ
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Seg pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Plant Pathology & Microbiology
Texas A&M University
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Strain incollated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
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Alignment Scores:

No.:

Percent Similarity:

7.04e-75 694.00 94.8%

Conservative:

Search completed: Job time : 4367 se	Qy 141 Db 563	Qy 121 Db 505	Qy 101 Db 445	Qy 81 Db 385	Qy 61 Db 325	Qy 41 Db 265	Qy 21 Db 205	Qy 1 Db 145	US-10-507-132-2	Best Local S Query Match: DB:
leted: December 1367 secs									(1-172) x	imilarity:
4, 2006,	ValTrpLysPheAlaGlyLeuLysProAspIleArgTrp 	ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyr 	3GlnLeuArgValP3 CAGCTGGGCGTCC	HisPheIleGlyG CACTTCATCGGCGG	IGluPheValGlyMe GAGTTCGTCGGCAS)ThrLeuArgIleAs ACTCTGCGCATTG <i>I</i>	:GluTrpAlaAspSe GAGTGGGCAGACAC	\ValGlnLysSerAs \GTTCAAAAGAGCG <i>I</i>	BM864472 (1-600)	94.1% N 73.7% 1
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US-10-507-132-3

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842.475 Million cell updates/sec
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Sequence 3, Appli
Sequence 1, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 14, Appl
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ALIGNMENTS

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RESULT 1 US-10-507-132-1

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Percent Similarity:
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                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: Koichiro KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE:

TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10

PRIOR FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: UF 2002-66955

PRIOR FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                        SEQ ID NO 1
                                                                                                                                                                  TYPE: DNA
ORGANISM: Pyricularia oryzae
FEATURE:
NAME/KEY: CDS
                                                                                                                                                        LOCATION:
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Matches:
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US-10-507-132-3
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Publication No. US20060223136A1
GENERAL INFORMATION:
APPLICANT: KOICHIV KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT APPLICATION NUMBER: J002-03-12
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR PILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 516
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ORGANISM: Pyricularia
FEATURE:
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                                                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/10507132 Publication No. US20060223136A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                             APPLICANT: KOICHIFO KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR PILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                            TYPE: DNA ORGANISM:
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Sequence 16, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION: CAKU et al.

APPLICANT: KOICHITO KAKU et al.

TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

FILE REFERENCE: 1254-0258PUS1

CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT APPLICATION NUMBER: US/10/507,132

CURRENT FILING DATE: 2004-09-10

PRIOR APPLICATION NUMBER: US/10/507,132

PRIOR PILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 19

SSOCTWARE: Patentin Ver. 2.1

LENGTH: 610

TYPE: DNA

ORGANISM: Pyricularia oryzae

US-10-507-132-16
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Best Local Similarity:
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CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 538
TYPE: DNA
ORGANISM: Pyricularia oryzae
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; Sequence 15, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUSI.
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US-10-507-132-2 (1-172) x US-10-507-132-14 (1-545)
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Best Local Similarity:
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Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: AGENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE '
TITLE OF INVENTION: AGENCULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 545
TYPE: DNA
ORGANISM: Pyricularia oryzae
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                    IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu
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Matches:
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Publication No. US20060223136A1
GENERAL INFORMATION:
APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1.254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: UP 2002-66955
PRIOR PILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 729
TYPE: DNA
ORGANISM: Pyricularia oryzae
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Best Local Similarity:
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sPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGl 105
                                             uPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHi 85
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US-10-507-132-17

(Sequence 17, Application US/10507132

(Publication No. US20060223136A1

(GENERAL INFORMATION:

APPLICANT: KOICHITO KAKU et al.

(TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO FITTLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

(FILE REFERENCE: 1254-0258PUS1

(CURRENT APPLICATION NUMBER: US/10/507,132

(CURRENT APPLICATION NUMBER: US/10/507,132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                  GACTGGGATAGGCTGCGAAAGGTCATTGCGCCCTACTCTGCGCGTATGTTCCGCCCTGCCA
                                                                                                                      AspTrpAspArgLeuArgLysVallleAlaProThrLeu-----
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             -ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla
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870.00
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74.2%
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Best Local Similarity:
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                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: OTYZA SATİVA
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK066825
DATABASE ENTRY DATE: 2001-12-06
                                                                                        2160
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APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

ITITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269

PRIOR RILING DATE: 2002-05-30

PRIOR RILING DATE: 2002-05-30

PRIOR RILING DATE: 2002-05-30

PRIOR RILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16327

LENGTH: 3196
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US-10-449-902-16327
; Sequence 16327, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      US-10-507-132-2 (1-172) x US-10-449-902-16327 (1-3196)
                                                                                    CGCCGCGGCATGGCCGAGGAGGACCCCACG-----GCGGAGCACGGCCTCAGGCTCGCC
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Matches:
-GlyGlyThrArgTrpGluLysVal---
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PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 3703
LENGTH: 1611
TYPE: NOS
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US-11-174-307B-3703
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Best Local Similarity:
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                                                                         US-10-507-132-2 (1-172) x US-11-174-307B-3703 (1-1611)
                                                                                                                       Query Match:
                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3703, Application US/11174307B Publication No. US20060143729A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
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                                                                                                                                                                                                                                           LOCATION: (1)..(1611)
OTHER INFORMATION: Also known
                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: (1)..(1611) OTHER INFORMATION: Ceres
                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)..(1611)
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Ceres
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                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                      LeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGly------
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                 TTGGCCAAGCTCAGGGAGTCG---
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Mismatches:
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               --ĠĊĊĠĀĠGCGTACCTCĠĠĊCGTGCAATCCAGGAG 621
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US-10-507-132-2 (1-172) x US-11-056-355B-70677 (1-1845)
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                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                Alignment Scores:
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LENGTH: 1845
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590BVS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ_ID NOS: 119966
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1845)
OTHER INFORMATION: Ceres
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                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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16 TyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAsp-----
                                       CAACCAAGTGATGAGGATCTTGGTACCATCATTGGACCTCATCAAACTAGCTTCGATGAC 144
                                                                             GlnLysSerAspGlu----
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SEQ ID NO 0
                                                                                                                                                                                                                                           Length:
Matches:
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Indels:
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RESULT 12
US-11-056-355B-78749
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                                                                                                                                                        NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 78749
LENGTH: 1848
                                                                                                                                                                                                      APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-02-13
                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1848)
OTHER INFORMATION: Ceres
 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1848)
                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
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RESULT 13
US-11-217-529-78037
| Sequence 78037, Application US/11217529
| Publication No. US20060099612A1
| GENERAL INFORMATION:
| APPLICANT: SUNTORY LIMITED
| APPLICANT: NAKAO, YOSHIHIRO
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Best Local Similarity:
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APPLICANT: KODAMA, YUKIKU
APPLICANT: APHICANT: TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF
FILE REFERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOPTWARE: PATENTIN VERSION 3.3
SOPTWARE: PATENTIN VERSION 3.3
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LENGTH: 2451
TYPE: DNA
ORGANISM: Saccharomyces pastorianus
US-11-217-529-78037
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RESULT 14
US-11-266-748A-85042
; Sequence 85042, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
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                                                                                                                                         IleAspGlyValTrpLysPheAlaGly-----LeuLysProAspIleArgTrpGlyGlu 155
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KODAMA, YUKIKO
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TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
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; NAME/KEY: misc feature
; LOCATION: (119)..(119)
; OTHER INFORMATION: n is
US-11-266-748A-85042
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SEQ ID NO 85042
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo Sapiens
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                                                                       CAAGTTCATGTGGGGAAACTGATTTGGTTCCAAAGAAAAGAAGGATTGTTGGGTTGCCCT
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Mulligan, Karl
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (998)..(998)
; OTHER INFORMATION: n is
US-11-266-748A-137853
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Query Match:
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US-11-266-748A-137853/c
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105402.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PRIOR DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
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SEQ ID NO 137853
LENGTH: 1116
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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NUMBER OF SEQ ID NOS: 483996
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APPLICANT: Mulligan, Karl
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ORGANISM: Homo Sapiens
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APPLICATION NUMBER: EP 04105484.2
FILING DATE: 2004-11-03
APPLICATION NUMBER: US 60/662,276
FILING DATE: 2005-03-14
APPLICATION NUMBER: US 60/700,293
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106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
                                         440 CTTCAGCCAGGAACCAAGTTTATCAAACCACTGGAGGATGAA--
                                                                                                               500 TCCGTTATGCCAATGCTCAGGGCAGCATTTGTGGATGAGAATTTGCCTGATGGGACTCAC
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Matches:
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 251
                                                                                                             GlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGlu-----
AAGCCTAGGGAGGGAAGGATACA 228
                         -----AspGlyArgGluThr 168
                                                        GGCCTAAGGCCG-
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|----AAATACAGGAAATGTACAGTG---GAGTGCAGACACAAAGCT 360
                                                        - GÉCAGCTGGGAGTGGAATCGCGCGAGTAAGTGCACC
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Search completed: December Job time : 632 secs 4, 2006, 22:06:05 This Page Blank (uspto)

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -Q='Abss/ABSSWEB spool/USI0507132/runat_04122006_143928_11899/app_query.fasta_1
-Q='Abss/ABSSWEB spool/USI0507132/runat_04122006_143928_11899/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCLE0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-MATRIX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HBAPSIZE=500 -MINLEN=0 -MAXIEN=2000000000 -HOST=abss06h
-USER=US10507132_@CGN 1 1_1334_@runat_04122006_143928_11899 -NCPU=6 -ICPU=3
-NO_MMAP -NGE_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEY TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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                                                        Score
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Match Length DB
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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Sequence 18936, A Sequence 93, Appl	equence 34924	equence 2755,	0	quence	equence 2121,	equence 361, F	equence 279,	2121,	139221	equence 445	e 1, Api	303,	\vdash	equence 1,	Sequence 4, Appli	4	79084,	Sequence 47161, A	1665, 7	equence 1699,	e 1700,	61451	2839	69,	36	equence 43,	equence 2		e 7	ر ا	μ,	e 1. 2	equence 221	quence 1699	equence 45,	ce 59,	equence 28662	equence 31125,	quence 8,	

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US-10-491-733-21

Sequence 21, Application US/10491733 Publication No. US20040219675A1

GENERAL INFORMATION:

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; SEQ ID NO 21
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-491-733-21
                                                                                                                                                                                    APPLICANT: Weislo, Laura J.

TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic TITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality FILE REFERENCE: 60127WOPCT CURRENT APPLICATION NUMBER: US/10/491,733

CURRENT APPLICATION NUMBER: 0034,501

PRIOR APPLICATION NUMBER: 60/334,501

PRIOR FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Syngenta Participations AG
APPLICANT: Sainz, Manuel
APPLICANT: Saimeron, John
                                                                                                                                                                SOFTWARE: PatentIn version 3.1
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Alignment Scores:

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FEATURE:

, NAME/KEY: misc_feature

, LOCATION: 388

, OTHER INFORMATION: n = A
,US-09-882-227-305
                                                                                                                                                                                  FILE REFERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 305
SEQ ID NO 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 305, Application US/09882227
Publication No. US20030158396A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in
TITLE OF INVENTION: Genome
                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (37)...(831)
                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                        TYPE: DNA
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Tomb, Jean-Francois
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Matches:
Conservative:
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Best Local Similarity:
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                   Alignment Scores
                                                         US-09-964-238-8
                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/964,238
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/449,285
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: PCT/EP98/03193
PRIOR FILING DATE: 1998-05-28
PRIOR PPLICATION NUMBER: 97201645.5
PRIOR PPLICATION NUMBER: 97201645.5
PRIOR PILING DATE: 1997-06-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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 Pred. No.:
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APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology
TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
FILE REFERENCE: 2676-4232US
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09964238 Patent No. US20020035246A1
                                                                                                               SEQ ID NO 8
LENGTH: 850
                                                                        TYPE: DNA
ORGANISM: Mus
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                                                                                       US-10-507-132-2 (1-172) x US-10-425-114-31125 (1-1454)
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
APPLICANT: Tabaska, Jack
                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31125, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                           TYPE: DNA
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45 ThrLeuArgIleAspTyrArgSerPhe---
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Screen, Steven E
Tabaska, Jack E
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                                      TGGAAAGACGTGTTTGATTCGGCAAGCTGGGAAGACCTGATTGTGCGGTATATCATTCCT
                                                             TrpAlaAspSerTyrAspSerLysAspTrp---AspArgLeuArgLysValIleAlaPro
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Best Local Similarity:
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US-10-425-115-28662
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SEQ ID NO 28662
LENGTH: 1454
TYPE: DNA
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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US-10-507-132-2 (1-172) x US-10-425-115-28662 (1-1454)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acid Molecule
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                        572 AAACTGAGATTGGCGTTGCAAGACTTTCAGATCAACCCAGCAAACCAGAAGCTCGATCAG 631
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45 ThrLeuArgIleAspTyrArgSerPhe-------
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Matches:
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                                                                                                    TTGGAAGTCGATTTCTTC-----AGC 709
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APPLICANT: ZOU, YIMIN

APPLICANT: ZOU, YIMIN

FILE REFERENCE: ARCD:395US

CURRENT APPLICATION NUMBER: US/10/847,972

CURRENT FILING DATE: 2004-05-17

PRIOR APPLICATION NUMBER: 60/470,913

PRIOR FILING DATE: 2003-05-15

NUMBER OF SEQ ID NOS: 85

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 59

LENGTH: 3154

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:
NAME/KEY: CDS

LOCATION: (133)..(1182)

US-10-847-972-59
RESULT 7
US-11-108-528-45
; Sequence 45, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
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Publication No.
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                                                                                                    GCCCGTGAG
                                                                                                                              GlyArgGlu 167
                                                                                                                                                                                      AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
                                                                                                                                                                                                                                                                                                        ThrMetLysGlyHisAlaHisSer-----
                                                                                                                                                                                                                                                                                                                                     GGG----CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC-----TATGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                        GlnHisPheIleGlyGlyThrArgTrp-----GluLysValSerGluAspGluValIle 101
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                                                                                                                                                          GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGCTTTGTGGAT
                                                                                                                                                                                                                    TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG
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No. US20050049195A1
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84.00
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Percent Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                    Sequence 1699, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION:
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LENGTH: 3154
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                 APPLICANT: MORRIS, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT FAPPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
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TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
TITLE OF INVENTION: PROLIFERATION
FILE REFERENCE: HYDR-P01-041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Mouse
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Chen, C. M. Amy
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Li, Dean Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-335-977-2219
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2219, Application US/10335977 Publication No. US20040052799A1 GENERAL INFORMATION:
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SEQ ID NO 1699
LENGTH: 88232
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1):...(88232)

OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26587 GGATACCACCAGGCCAGA 26604
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SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 GlyTyrHisGlnLeuArg 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAACTGGAGGTGGTTTGAAATCTGGCACTCATTTTCTAGGACTCAGAGCAGGGACTGTGG 26586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgTrpGluLysVal------
                                                                                                                                                                                                            ZIP: 02109-1875
                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                    STREET: 28 State Street
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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Conservative:
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; Sequence 1, Application US/10364888; Publication No. US20040023259A1; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca; APPLICANT: Zhong, Haihong; APPLICANT: Boldog, Ferenc; APPLICANT: Gangolli, Esha; APPLICANT: Guo, xiaojia; APPLICANT: Malyankar, Uriel
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Best Local Similarity:
Query Match:
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US-10-364-888-1
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INFORMATION FOR SEQ ID NO: 2219:
SEQUENCE CHARACTERISTICS:
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LOCATION: (B) LOCATION 1...1473
SEQUENCE DESCRIPTION: SEQ ID NO: 2219:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                               460
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                                                                                                                                                                                                                                                                                                                                                                                                                  103 TyrHisGln-LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValTh 122
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                                                                                                                                                                                                                                                                 pGlyValTrpLysPheAla-----GlyLeuLysProAspIleArg 152
                                                                                                                                                                                                                                                                                                                                         rMetLys-----GlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIle----As
                                                                                                                                                                                                                                                                                                                                                                               CATGTTGATCATGGTAATACCTCACTACTGGATAAAATCCGTGATAAGAGAGTCGCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGly 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
                                                                                                                                                                                                                               TGGGTGTCTTTCATTGACACCCCAGGGCATGAAGCCTTCAGCCAGA
                                                                                                                                                                                                                                                                                                        ACTGAAGCCGGGGGATCACTCAGCACATTGGTGCTTACATGGTGGAAAAAATAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGAAGAGTTTCATTTAGAAATTTCTGTTCAAAACACCTTAGAAGAA-----TTTGAA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
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36,207
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Matches:
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Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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; LOCATION: (1)
US-10-364-888-1
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                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                       Sequence 1, Application US/10305810 Publication No. US20030176385A1
                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Rieger, Daniel
APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2000-07-26
RUMBER: OP SEQ ID NOS: 14
                   APPLICANT:
                                                                                                                                     APPLICANT: Ju, Jingfang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                             469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
 Huang, Chunli
Zhong, Haihong
Simons, Jan Fredrik
Tailon, Bruce E.
Chant, John S.
Peyman, John A.
Smithson, Glennda
Millet, Isabelle
                                                                                                                                                                                                                                                                                                                            CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĊĠĊŦĠĠAACTGCTCTGCCCTCGGCĠÁĠAAGACCĠŦĊTTCĠĠĠ---CAAGAGĊŦĊĊĠÁĠŦĀ
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                                                                                                                                                                                                                                                                                         ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
                                                                                                                                                                                                                                                                                                                                                            -----TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                                                                                                                                                                                                                                                                                                                                                                                                                              Ser-----AlaAsnLeuHis------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgTrp-----GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal
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Matches:
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Indels:
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GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
APPLICANT: Zhong, Haihong
APPLICANT: Boldog, Ferenc
APPLICANT: Gangolli, Esha
APPLICANT: Guo, Xiaojia
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US-10-364-888-5

Sequence 5, Application US/10364888 Publication No. US20040023259A1

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; TYPE: DNA
; ORGANISM: WNT-7B
US-10-305-810-1
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Query Match:
RESULT 12
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PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/192,838
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/194,256
PRIOR FILING DATE: 2000-04-03
PRIOR PILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
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LENGTH: 1070
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PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/970,813
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/182,637
PRIOR FILING DATE: 2000-02-15
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CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/334,148
PRIOR FILING DATE: 2001-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: CuraSeqList version 0.1
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                                           469
                                                                                  152
                                                                                                                            412 CAGGGCTACTÁCAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGÁCGTG
                                                                                                                                                                                                          352
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                                                                                                                                                                                                                                                                                                                                   109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis
                                                                                                                                                                                                                                                                                                                                                                                241 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                     91 ArgTrp-----GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
                                         CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 513
                                                                                ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
                                                                                                                                                               -----TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle
                                                                                                                                                                                                          GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG
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Matches:
Conservative:
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Indels:
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; TYPE: DNA; ORGANISM: Homo s; PEATURE; PEATURE; CDS; LOCATION: (1)...(US-10-364-888-5
              Sequence 7, Application US/10364888
Publication No. US20040023259A1
GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
APPLICANT: Zhong, Haihong
APPLICANT: Boldog, Ferenc
APPLICANT: Gangolli, Esha
APPLICANT: Guo, Xiaojia
APPLICANT: Malyankar, Uriel
APPLICANT: Patturajan, Meera
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US-10-364-888-7
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CURRENT FILING DATE: 2003-02-12
PRIOR APPLICATION NUMBER: 60/356,375
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR APPLICATION NUMBER: 60/625,634
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 14
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APPLICANT:
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APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 15966-744CIP
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 APPLICANT
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Patturajan, Meera
Pena, Carol
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Matches:
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; Publication No. US200
; GENERAL INFORMATION;
; APPLICANT: Rhee, Cha
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APPLICANT: Edinger, Shlomit
APPLICANT: Burgess, Catherine
TITLE OP INVENTION: THERAPBUTIC POLYPEPTIDES, NUCLEIC FILE REFERENCE: 15966-744CIP
CURRENT APPLICATION NUMBER: US/10/364,888
CURRENT FILING DATE: 2003-02-12
              APPLICANT: Leoni Lorenzo M.
APPLICANT: Corr, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
APPLICANT: What and Frizzled Receptors as Targets for I
TITLE OF INVENTION: in Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-130320US
                                                                                                                APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenz
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PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/387,082
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR APPLICATION NUMBER: 09/625,634
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CURRENT APPLICATION NUMBER: US/10/285,976
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LOCATION: (6)
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ORGANISM: Homo
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Vernet, Corine
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No. US20030165500A1
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Matches:
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CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995
PRIOR FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: WO PCT/US02/13802
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 232
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 22
LENGTH: 2250
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US-10-847-972-21
                                                Alignment Scores:
Pred. No.:
                                                                                                 ; NAME/KEY: CDS
; LOCATION: (96)..(1145)
US-10-847-972-21
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Best Local Similarity:
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; ORGANISM: Homo sapiens
; PEATURE:
; OTHER INFORMATION: human wnt-7b
US-10-285-976-22
Percent Similarity:
Best Local Similarity:
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                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 2250
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20050049195A1
GENERAL INFORMATION:
APPLICANT: ZOU, YIMIN
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: ARCD:395US
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/847,972
CURRENT FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/470,913
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEQ ID NOS: 85
                                                                                                                                                     FEATURE:
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                     ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
                                                                         -----TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle
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Search completed: December Job time : 912 secs 4, 2006, 20:27:11

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us-10-507-132-2.p2n.rni
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OM protein - nucleic search, using frame_plus_p2n model Run on: December 4, 2006, 19:19:24; Search time 143 Seconds Title: US-10-507-132-2 Perfect score: 942 Sequence: 1 MGSOVQKSDEITFSDYLGIMWGEFDPDRIFEDGRETFGDK 172 Secoring table: BLOSUM62 Sequence: 1 MGSOVQKSDEITFSDYLGIMWGEFDPDRIFEDGRETFGDK 172 Secoring table: BLOSUM62 Searched: 1403666 seqs, 935554401 residues Total number of hits satisfying chosen parameters: 2807332 MAXIMUM DB seq length: 0 MAXIMUM DB seq length: 0 MAXIMUM DB seq length: 10004 MAXIMUM DB seq length: 10004 MAXIMUM DB seq length: 10004 MAXIMUM DB seq length: 0 MAXIMUM DB seq length: 0 Delber	GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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77	79 77	81	9 0	84	84	94.5	Score
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US-09-252-991A-12501	US-10-149-736-4	US-09-625-634A-1	US-09-543-681A-477	TIS-09-964-238-8	US-09-449-285A-8	US-09-328-352-44	ID
Sequence 12501, A	Sequence 4, Appli		Semience 477 Ann		ω.	Sequence 44, Appl	Description

ALIGNMENTS

US-10-507 Qy Db	Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB:	RESULT 1 US-09-338-352-44 Sequence 44, A Patent NO. 656 Patent NO. 656 GENERAL INFORM APPLICANT: GA TITLE OF INVE TITLE OF INVE FILE REFERENC CURRENT APPLI CURRENT FILIN NUMBER OF SEO SEQ ID NO 44 LENGTH: 462 TENE: DNA ORGANISM: AC US-09-328-352-44
US-10-507-132-2 (1-172) x US-09-328-352-44 (1-462) Qy	ores: larity: imilarity:	SSULT 1 :09-328-352-44 :09-328-352-44 Sequence 44, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION: APPLICANT: GARY L. Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND AMIN TITLE OF INVENTION: BAUMANNII FOR DIAGNOS FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 44 LENGTH: 462 TYPE: DNA ORGANISM: Acinetobacter baumannii :09-328-352-44
x US-09-328-35 ilyLeuMetThrCys :::::: :GTATTTTAGAGGTC	0.00957 94.50 43.7% 23.0% 110.0%	ion US/09328352 ion US/09328352 ieton et al. iUCLEIC ACID AN AUMANNII FOR D i-03PA iUMBER: US/09/3 1999-06-04 8252 iter baumannii
2-44 (1-462) ValTyrGluTrpAla ::: ATTACGCGTTTTCAA	Length: Matches: Conservative: Mismatches: Indels: Gaps:	ULT 1 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44 109-328-352-44
32-2 (1-172) x US-09-328-352-44 (1-462) 15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34	462 31 28 59	ULT 1 09-328-44 09-328-352-44 equence 44, Application US/09328352 atent No. 6562958 atent No. 6562958 atent No. 6562958 ENERAL INFORMATION: APPLICANT: Gary L. Breton et al. APPLICANT: Gary L. Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUWANNI FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 EQ ID NO 44 LENGTH: 462 TYPE: DNA ORGANISM: Acinetobacter baumannii 09-328-352-44

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APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology
TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
FILE REFERENCE: 2676-423US
CURRENT APPLICATION NUMBER: US/09/449,285A
CURRENT FILING DATE: 1999-11-26
CURRENT FILING DATE: 1999-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8
LENGTH: 850
TYPE: DNA
ORGANISM: Mus musculus
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Patent No. 6313280
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 97201645.5
PRIOR FILING DATE: 1997-66-02
NUMBER OF SEQ ID NOS: 27
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                                  TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG
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AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp
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RESULT 4
US-09-543-681A-477
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DB:
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Best Local Similarity:
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/449,285
PRIOR FILING DATE: 1999-11-24
PRIOR APPLICATION NUMBER: PCT/EP98/03193
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 97201645.5
PRIOR APPLICATION NUMBER: 97201645.5
PRIOR FILING DATE: 1997-06-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
Sequence 477, Application US/09543
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID
TITLE OF INVENTION: DIAGNOSTICS
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TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SMAD-INTERACTING FILE REFERENCE: 2676-4232US
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      AND AMINO ACID SEQUENCES RELATING AND THERAPEUTICS
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Matches:
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APPLICANT: Vernet, Corine
APPLICANT: Rastelli, Luca
APPLICANT: Herrmann, John
TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND
TITLE OF INVENTION: SAME
FILE REFERENCE: CURA-244 (15966-744) US
CURRENT APPLICATION NUMBER: US/09/625,634A
CURRENT FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: USSN 60/194,256
PRIOR APPLICATION NUMBER: USSN 60/194,256
PRIOR APPLICATION NUMBER: USSN 60/192,838
PRIOR APPLICATION NUMBER: USSN 60/192,838
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CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 477
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           sequence 1, Application US/09625634A Patent No. 6653448
 SOFTWARE:
                   NUMBER OF
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ORGANISM: Proteus mirabilis
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PatentIn
                 SEQ ID NOS:
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; NAME/KEY: CDS
; LOCATION: (1).
US-09-625-634A-1
US-10-507-132-2 (1-172) x US-10-149-736-4 (1-11096)
                                    Query Match:
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                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 11096
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CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: PCT/US01/31126
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,848
PRIOR APPLICATION NUMBER: 60/238,848
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Harper, Scott Q.
TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
FILE REFERENCE: UM-06968
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                                                                                                                                                                           ORGANISM: Mus musculus
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15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp

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Percent Similarity:
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12976
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PRIOR FILLNG DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12976
LENTH: 687
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Patent No. 6551795
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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No.:
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 78 AspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp--
                                           GAAGATCAGCCAGCCGAACAGCGCCTTGGTCAGCGCGTTGCTCCAGGACATATCCTGGGC
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DB:
                                          WS-09-252-991A-13297/c
US-09-252-991A-13297/c
; Sequence 13297, Application US/09252991A
; Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12501
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US-09-252-991A-12501
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GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION:
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                                                                                                                  661 GAGTCGATTCATCGCAGCGTTCTCCAC
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Rubenfield et
NUCLEIC ACID
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77.00
44.9%
28.1%
8.2%
al. AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Matches:
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Indels:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
FILL REFERENCE: 107136.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12501
LENGTH: 2103
TYPE: DNA
                                                                                                                                GCCGAGGTCGTAGAACAGGGTGAAGACGTTGGTCATCACCACATAGAGGAAGGTCACCAG
                                                                                                                                                                                           ---GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln
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CGTCATCGCCGCCAGCAGGAAGGCGATAGCGCCCTCCTCGAAGCGGTTCCAGACGCGCAC
                                                          ArgTyrLys-----AspThrThrMetLysGluValThrMetLysGlyHis 126
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-00

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16153
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Best Local Similarity:
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  Score:
                                                                                         ; ORGANISM: Human US-09-949-016-16153
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                        Pred. No.:
                                         Alignment Scores:
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13297
LENGTH: 3045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16153, Application US/09949016 Patent No. 6812339
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CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                          LENGTH:
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ULT 11 09-248-7 equence atent No eneral I APPLICAN TITLE OF FILE REF FILE REF CURRENT CURRENT CURRENT PRIOR AP PRIOR AP	13341	170	13284	153	13224	139	13183	119	13149	99	84 13089	1	68 13029	12978	48	43 12918	12858	42	12798	38	18 12738	12678	1	10-507-132	Best Local Si Query Match: DB:
8 37 37 37 10N: h weins 10N: NU 110N: F 110N: F 110N: NU DATE: ON NUMB ON NUMB ON NUMB	GGCCAAAA 1334	lyAspLys 172	GGGCGTCTCTTG	rp	CTGGCTGCTGGA	spGlyValTrpLysPhe	1	sGluValThrMe	GGTCTGTGGGCT	uValIleGlyTy	Gln-HisPheIl TCTGGACCTCAT		GlyMetValSerSer	::: ATCAGTAGAAAA	IleAspTyrArg	ATGTGGCTGGGG	AGCGTGTACTTG	:	CTGTGTGTTGCT	LeuArgLysVal	GlyLeuMetThrCy	ATGGGAAGCAGA	MetGlySerGln	-2 (1-172) x	Similarity: 23 h: 8.
L-1708 18, Application US/09248796A 7747137 7747137 Keith Weinstock et al WENTION: NUCLEIC ACID AND A WENTION: FOR DIAGNOSTICS A NCE: 107196.132 LICATION NUMBER: US/09/248, LING DATE: 1999-02-12 IG DATE: 1998-02-13 48		GCCTCTGGTCCTA	lyGluPheAspPh	GCCTCTGCCCCTG	ysPhe	 GCCCATGCA	sGluValThrMetLysGlyHisAlaHisSer-	GGTCTGTGGGCTAGGATGGCTGGGCTTCCCCCAT	rHisGlnLeuArg	Gln-HisPheIleGlyGlyThrArgTrpGlu- ::: TCTGGACCTCATTTCTTCTGTACGCTGGGATT		SerLysc	::: CATGGTTGCCTA	gSerPheLeuAspLy	TTGGCTTCAGCCT	TGTGAGCGTGTGG		::: GTGTGGGAATGGA	.Ile	CysValTyrGluTrpA GTGTGTACATCTGGG	GCATCCATGTCGA	ValGlnLysSerA	US-09-949-016	23.0% 8.1% 3	
6A AMIN AND 8,796 8,796			GGCGTCTCTTGGCCTCTGGTCCTACCCAGGCCTGCTG	GlyGluPheAspPheAspArgIlePheGluAspGly	::: CCTCCGGGGCTCA	Ala	GCCCATGCACTGCCTGGCCAGGCTC-	Hisser-AlaAsn	TTCCCCCAT	ValProHisGlnA	TrpGlu ::: TGGGATTGTAATO		lnMetLeuGlyAs ::: GTTTGCTGGGTGA			CAGGCCTGTGGCT	CTACTGGGCATGG	1	CTGCTGTGGTTTG		PA1	GCCGTGCATTTAC	MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAs	-16153 (1-24070)	Mismatches: Indels: Gaps:
O ACID SEQUENCES RELATING THERAPEUTICS A			GATGGGAGGAAACTTTTC	ArgG		AlaGlyLeuLysProAspIleArgT	 CTCCTGAGAAGGCCTGTCC	AlaAsnLeuHisTrpTyrLysLysIleA		TyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLy	Gln-HisPheIleGlyGlyThrArgTrpGlu		GlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 	 GTCCCCGGAT	sLeuTrpGluAlaMetProAlaGluGluPheVa	AlaProThrLeuArg ::: ATGTGGCTGGGGTTGGCTTCAGCCTCAGGCCTGTGGCTTCCACATGCACCCTCCCGGGCC	AGCGTGTACTTGTGTGAGCGTGTGGCTACTGGGCATGGGCATGCCTGTGCGTGTATGGAC		 CTGTGTGTTGCTGTGTGGAATGGACTGCTGTGGTTTGTCTGGTGCCTGAGGGCCTAGGG		pAlaaspSerTyraspSerLysaspTrpasparg decgrototototototototocogtogaartot	::: ATGGGAAGCAGAGCATCCATGTCGAGCCGTGCATTTACGAGCAGTCGTGCAGCCATGTGC	p	70)	79 91 11
TO CANDIDA			 TTCC 13340	cPheG 170	 CATTT 13283	eArgT 153	::: rGTCC 13223	3IleA 139	13182	MetLy 119	1spGl 99 3GGGA 13148	: ;	CCTC 13088	 GTG 13028	neVal 67	euArg 47 EGGCC 12977	rGGAC 12917	42	MGGG 12857	42	spArg 37 :: ATTGT 12797	rGTGC 12737	TyrLeu 17		

ALBICANS

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Sequence 97, Application US/09614221A
Patent No. 6723837
GENERAL INFORMATION:
APPLICANT: Karunanandaa, Balasulojini
APPLICANT: Yu, Jaehyuk
APPLICANT: Yishore, Ganesh M.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AN
TITLE OF INVENTION: WITH STEROL SYNTHESIS AN
TITLE OF INVENTION: WITH STEROL SYNTHESIS AN
TITLE OF INVENTION INVERSE: US/09/614,221A
CURRENT APPLICATION NUMBER: US/09/614,221A
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Query Match:
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PRIOR APPLICATION NUMBER: US 60/142,981
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 626
SEQ ID NO 97
LENGTH: 1776
TYPE: DNA
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NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1708
LENGTH: 1806
                                                                                                                                                                                                                                                                    784 GACTTGAAAAACCAAAGAACTCACCTTA 811
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                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                              1513 GCCCGTCCTGGTTACAGG
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                                                                                NUMBER OF SEQUENCES:
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                CITY: Rockville
STATE: MD
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    COUNTRY: USA
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Matches:
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US-10-507-132-2 (1-172) x US-09-614-221A-97 (1-1776)
              S-09-557-884-1/c
Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influence of the Haemophilus influence of the Haemophilus influence
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COMPUTER READABLE FORM:

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Best Local Similarity:
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                                                                                                                                                                                                                                                                          227481 AGTGAAACTCGTCCATTGAAATTACGT-----ATTCGTTATGATGATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227652 AAAAGTGCGGTAAGAAAAGCGÁTTGTTTCGATGATTTCTACCAATAATTTGGTTGCAGAT 227593
                                                       227316 TTTCAATTAATTCGTTCTGGCTGGTGTGCTGATTTTAATGATCCTGCAGCATTTCTAAAT 22725
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION IMFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
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                                                                                         AlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGly
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--LysProAspIleArgTrpGly-----GluPheAspPheAspArg
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Matches:
Conservative:
Mismatches:
Indels:
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35 TrpAspArgLeuArgLysVallleAlaProThrLeuArglleAsp---::::

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US-09-643-990A-1/c
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                                       US-10-507-132-2 (1-172) x US-09-643-990A-1 (1-1830121)
                                                                                                 Query Match:
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Patent No. 6528299
GENERAL INFORMATION:
APPLICANT: Robert D. Fleischma
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/487,429
FILLING DATE: 1995-04-07
APPLICATION NUMBER: 08/426,787
FILLING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P10
TELEPHONE: 301-610-5790
TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227256 TTATTCTATTCAAAAAGCCCAGATAACAAAAATGGCTATAAAAATGCGGAATTTGATCGT 227197
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
   15
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COUNTRY: U
AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp
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                                                                                                                                                                                                                                                                      STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton O. Smith
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RESULT 15
US-10-158-865-1/c
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Patent No. 6846651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Patent No. 6846651
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR ETLING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR ETLING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PB186P2C1D1
CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fleischmann et al.
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1
                                                   FEATURE: NAME/KEY: misc_feature LOCATION: (10150)...(10150) OTHER INFORMATION: n equals
                                                                                                                         NAME/KEY: misc feature
LOCATION: (9921)...(9921)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                    ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                        TYPE: DNA
                                          FEATURE
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(29298)..(29298)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATTCTATTCAAAAAGCCCCAGATAACAAAAATGGCTATAAAAATGCGGAATTTGATCGT 227197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHis 126
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NAME/KEY:
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals
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LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (55369)...(55369)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51602)...(51602)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (51334)...(51334)
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NAME/KEY: misc_feature
LOCATION: (45732)...(45732)
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LOCATION: (45593)..(45593)
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LOCATION: (44975) .(44975)
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LOCATION: (36551)..(36551)
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LOCATION: (51805)..(51805)
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LOCATION: (51786)..(51786)
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LOCATION: (44905)...(44905)
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LOCATION: (44416)...(44416)
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NAME/KEY: misc feature
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LOCATION: (131360)...(131360)
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OTHER INFORMATION: n equals
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LOCATION: (122167)...(122167)
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LOCATION: (119750)..(119750)
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LOCATION: (117136)..(117136)
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a,t,
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OTHER INFORMATION: n equals
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LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals
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LOCATION: (140398). (140398)
OTHER INFORMATION: n equals a,t,
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LOCATION: (121344)..(121344)
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LOCATION: (119924)..(119924)
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LOCATION: (102696)..(102696)
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LOCATION: (100091)..(100091)
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-MODBLE-frame+ p2n.model -DEV=Xlp
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-DB=N Geneseq -QFWT=fastap -SWFFIX=p2n.rng -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 516 BP; 119 A; 151 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a gene encoding scytalone dehydrogenase (SCDH that functions in the presence of an inhibitor, comprising an optional mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors a evaluating sensitivity to them. The current sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 516
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                                            The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the scytalone dehydrogenase DNA sequence. Note: gene sequence from this is given in ADC16590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 610 BP; 148 A; 179
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(NARE-)
(NORQ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of fermentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-046817/04.
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                               GAAAAAAACGTAAGGGTTGTTTTTCAAATCATGGCGGTTCATCGGAGGGCGCCAAAAGAC
                                                                            GGGAACCCCGATATCCAGTGACATCATTTATCGGTGCCTGCAAATGGGCACGGGAACTG
                                                                                                 GlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSer
                                                                                                                           AAGGCTACCGCTGTGGAGTTTTCTGTTTTTATCGAACACTACTCCAGTTCAGCACAGCTA
       ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys
                                                    GluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThr
                                                                                                                                                LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeu 76
                                                                                                                                                                         CGTATGCTGACTATATTCGCGCCCCAGAATCGATGTGGATTACTCGGCGGTCGGGACACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akita O, K
Kobayashi
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183.00
47.9%
28.8%
19.4%
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423

303

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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic, oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polynucleotides stringently hybridising to these sequences. The polynucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus oryzae; fermentation; fungus; industrial; EST; expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                           184 CTCGCATGTNAGAACCTCCTTCACGACTGGGCAAACTGCTTAGACACCAAGTCCTGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAT INST ADVANCED IND SCI & NAT RES INST BREWING.
NAT FOOD RES INST MIN AGRIC
                                                                                                LeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1679; 48pp +
ArgLeuArgLysVallleAlaProThrLeuArglleAspTyrArgSerPheLeuAspLys 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression of specific Aspergillus grand growth conditions of the fungus,
                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 170 A; 153 C; 180 G; 189 T; 0
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i T, Kitamoto
                                                                                                                                                                       (1-697)
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Matches:
Conservative:
Mismatches:
Indels:
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N, Gomi
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Abe K;
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                                                                     US-10-507-132-2 (1-172) x ADA28757 (1-462)
                                                                                                                                                           Percent Similarity:
                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                  The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                   Sequence 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998;
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DB; ADA32883.
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                                                                                                                                          Similarity:
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GACTACCATCGTATTTTAGAGGTCATTACGCGTTTTCAATTGGTTTTTGACCAGAAAAAT
                          AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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ABB42401_07
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MetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLys
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         The invention relates to nucleic acid molecules from rice encoding proteins for abiotic stress tolerance, enhanced pathogen or disease resistance and altered nutritional quality. The sequences of the invention are useful for altering abiotic stress tolerance, pathogen or disease resistance or the grain quality, nutritional content or yield in a plant. The present sequence is rice disease resistance gene, LOX1
                                                                                                                                                                                                                                                                      New nucleic acid from Oryza sativa, useful for altering abiotic stress tolerance, pathogen or disease resistance or the grain quality, nutritional content or yield in a plant.
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                                                                                                                                                                                                                                                                                                                                           Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                                                                                      detection; infection; Antibacterial;
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Buchrieser C,
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    Legionella pneumophila
                                           detection; infection; Antibacterial; Vaccine;
                                                                                          L. pneumophila DNA SEQ ID NO 42.
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24-JUN-1997;
29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infection including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection is diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Helicobacter the diagnosis, prevention gastrointestinal diseases.
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                                                                                                                                                                                                                                                                                                                                           35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu
                                                                                                                                                                                                                                                                                                                                                                                              18 GlyLeuMetThrCysValTyrGlu-----TrpAlaAspSerTyrAspSerLysAsp
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GluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAsp |||||||| :::|||||||||
                                                                                                                                                   CGCTCTTACCCGCTCAAAGGCGATGAATTCGCCCAATGGTATGAAGTGGATAAAATTTTT
                                                                                                                                                                                                        AAACACCCCTATTTGAAACGCCTTATTATGCCGCATGATTGGGTAGGCCACCCATTATTG
                                                                                                                                                                                                                                                                                       AspLysLeu----TrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer
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                                        AAAGACACTTTCAATTTTGCAAAAATTGGCTATGAACAGGGCCAAGGGCGAAGAATTAAAA
                                                                                                                                                                            ArgThrGlnHisPheIleGlyGly-----ThrArgTrpGluLysValSerGlu-----
                                                                                              GGTAAAGAATACCGAGAAGTGGTGGGTAAAGAGCAGAGAGACAGCGCAAGAGTGGATGAA
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                                                                -LeuArgValProHisGlnArgTyrLysAspThrThrMetLys
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Query

US-10-507-132-2

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x AAV72504 (1-850)

Percent Similarity: Best Local Similarity:

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Conservative: Mismatches: Indels:

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                                                                         CC CDNA, designated SIP7. By using Smadl C-domain fused to GALA DNA-binding CC domain and a mouse embryo cDNA as bait and prey, respectively, in a two-cc hybrid screen, a partial Smadd and Smad interacting protein cDNAs (see CC AAV72502-05 and AAV72512-25), were obtained, including SIP1 (see CC AAV83318). The invention also provides recombinant expression vectors, CC transfected or transduced cells, a method of screening for compounds which affect the interaction between SMAD and SMAD interacting protein, CC transgenic animals useful for testing medicaments and as therapy models, CC and a method for post-transcriptional regulation of gene expression by CC members of the TGF-beta superfamily by manipulation or modulation of the interaction between Smad function and/or activity and mRNA stability.

CC SIPs and nucleic acids encoding them are useful therapeutically and in CC claimed kits for diagnosing diseases one metabolism related diseases CC or disorders and diseases affecting organs such as skin, lung, kidney, CC pancress, stomach, gonad, muscle or intestine. (Updated on 20-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for diagnosing neural disease.
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   Sequence 850 BP;
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ral disease; immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises a novel SMAD interacting protein partial By using Smadl C-domain fused to GAL4 DNA-binding
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   The invention relates to new Proteus mirabilis polypeptides and polypucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polypucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for plants.
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Search completed: December Job time : 599 secs 4. 2006, 20:48:11

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Minimum DB
Maximum DB
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-Q=/abss/ABSSWEB spool/US10507132/runat_04122006_143856_11163/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10507132/runat_04122006_143856_11163/app_query.fasta_1
-DB=GenEmbl -QFWFisep2n.rge -MINWATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -THR MX==100 -THR MIN=0 -ALICN=15 -MODE=LOCAL
-OUTFMT=pto -NORW-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss07
-USER=US10507132_0CGN 1_1_5548_@runat_04122006_143856_11163_-NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WAEN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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ALIGNMENTS

REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT 1
AB004741
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DEFINITION FEATURES COMMENT VERSION ACCESSION JOURNAL PUBMED Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Miclobial Toxicology Lab.; 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan (B-mail:tmotoyam@postman.riken.go.jp, Tel:+81-48-467-9518) Sequence updated (27-Oct.1998). Biosci. 9571787 CDNA scytalone dehydratase; sdhl. Magnaporthe grisea Magnaporthe grisea Magnaporthe grisea mRNA AB004741 needed for Motoyama, T., Imanishi, K. and Yamaguchi, I. Eukaryota; Fungi; Ascomyo Sordariomycetes incertae Direct Submission Motoyama,T AB004741.1 GI:3798733 (bases 1 to 807) (sites) cloning, expression, and mutagenesis of scytalone ed for pathogenicity of the rice blast fungus, Pyri Biotechnol. Location/Qualifiers Ascomycota; Pezizomycotina; Sordariomycetes; ncertae sedis; Magnaporthaceae; Magnaporthe. Biochem. 62 (3), 564-566 (1998) 807 scytalone dehydratase, ģ mRNA linear PLN 13-NOV-1998 complete cds. dehydratase

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          AB100172 77
Bipolaris oryzae BSCD1gene
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                                                                                                         IlePheGluAspGlyArgGluThrPheGlyAspLys
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                                                                                            ATCTTTGAGGACGGACGAGACCTTTGGCGACAAA
                                                                                                                                           GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG
                                                                                                                                                                                        GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
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TIRIDYRSFLDKLWEAMPAEEFVGMVSSKQVLGDPTLKTQHFIGGTRWEKVSEDEVIG
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whose telemorphic form is unknown"
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/mol_type="mRNA"
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US-10-507-132-2 (1-172) x AB100172 (1-770)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning, functional analysis and expression of a scytalor dehydratase gene (SCD1) involved in melanin biosynthesis phytopathogenic fungus Bipolaris oryzae curr Genet. 45 (4), 197-204 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bipolaris oryzae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerGlnValGlnLysSerAspGluIleThrPheSerAspTyr------LeuGly
LysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIle
                                                GAGATTACGGGATACCACCAGCTGCGAGTGCCTCACCAGCGATACACGGATGAGTCACGG
                                                                           GluVall1eGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMet
                                                                                                                                          CCCCTCCTCAAGACACAGCACTTCATCGGCGGAACACGGTGGGAGAAGACGGCCGAGGAT 375
                                                                                                                                                                ProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAsp
                                                                                                                                                                                                                                  GAGGCGATGCGAGCGGATGAGTTTGTGGCCATGGCCTCTGACCCTGCGGTGCTCGGCAAC
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Clrvehqrytdesrativavkghahernthwykkidgemkfaglnpdirwyeydfdkvf
Aegreolgeakaaagipetapgqav"
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join(34. .70,125. .645)
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Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.

1 (bases 1 to 1477)

Wang,H.L., Kim,S.H. and Breuil,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A scytalone dehydratase gene from Ophiostoma floccosum restores the melanization and pathogenicity phenotypes of a melanin-deficient Collerotrichum lagenarium mutant Mol. Genet. Genomics 266 (1), 126-132 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-OCT-2000) Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada Location/Qualifiers
1. 1477
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Ophiostoma floccosum
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    TrpAspArgLeuArgLysValIleAlaProThrLeuArgIle----
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                                  GACTACATGGGCCTCTGCAGTGCCGCCTACGAGTGGGCCGACAGCTATGATTCCAAGGAC
                                                               AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1477)
                                                                                             (1-172)
                                                                                                                                                                                                                                                             /translation="MCLNISSLTSTTSSAPKTTGSDISFEDYMGLCSAAYEWADSYDS
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RWERISDTEVVGYHOLRYDHOYYTDTTLTQVAYKGHAHSANTHWYRKVDGVWKFASLD
PKIRWFEYDFDKVFASGRDQFGTEEKAAATAGPELLAKDKVQSAIASAQRAVAVSA"
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/gene="OSD1"
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/gene="OSD1"
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/protein_id="AAK11296.:
/db_xref="GI:12964738"
                                                                                                                                                                                                                                                                                                                                                                           /gene="OSD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Ophiostoma floccosum"
/mol_type="genomic DNA"
/strain="387N"
/db_xref="taxon:104300"
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join(316. .394,471. .571,635. .1
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                                                                                                                                                                                                                                                                                          Submitted (08-JAN-2003) Wood Science, Columbia, 4041-2424 Main Mall, Vancou
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 /product="syctalone dehydratase
/protein_id="AAO60167.1"
/db_xref="GI:37787190"
                                                                                                                                                                      /country="Canada:
                                                                                                                                                                                      /specific_host="Pinus contorta"
/db_xref="taxon:95837"
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/mol_type="genomic DNA"
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                                              codon_start=1
                                                                            product="syctalone
oin(233. .305,379.
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/gene="SD1"
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                                                                                                                                                                                                Direct Submission.

Submitted (22-APR-2002) Wood Science,

Columbia, 4th Floor, 2424 Main Mall, 1
                                                                                                                                                                                                                            Fleet, C. and Breus
Direct Submission
                                                                                                                                                                                                                                                                                                                   Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
1 (bases 1 to 427)
                                                                                                                                                                                                                                                        Fleet, C. and Breuil, C. Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)

2 (bases 1 to 427)
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-507-132-2 (1-172) x AY098656 (1-427) 121 CTAACAGACÁGATC-GÁCTÁCCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCC Aspergillus fumigatus
Aspergillus fumigatus
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

1 (bases 1 to 1447)
Teai, H.F., Washburn, R.G., Chang, Y.C. and Kwon-Chung, K.J.
Aspergillus fumigatus arpl modulates conidial pigmentation and
complement deposition
Mol. Microbiol. 26 (1), 175-183 (1997) Tsai,H.F., Wheeler,M.H., Chang,Y.C. and Kwon-Chung,K.J. A developmentally regulated gene cluster involved in copigment bloogynthesis in Aspergillus funigatus J. Bacteriol. 181 (20), 6469-6477 (1999) Aspergillus GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr ACTCTGCGAGTACGTCTTATACAACCCTGCTTTCTCTATTAACCCCATAAAGATCTTCTTG HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet PheAla 145 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLys GAAGAGTTTATCGGCATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACA GluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr ------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla ThrLeu-----CATCAGCTGCGCGTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTC CAACACTTCTTCGGCGCCTCGCGCTGGGAGCCCATCTCCGACACCGAGGTCGTGGGCCTAC (bases 1 to 1447) (bases 1 to 1447) 425 GI:2555059 5.24e-5 499.00 74.6% 64.1% 53.0% fumigatus .24e-53 scytalone 1447 Conservative: Mismatches: Indels: åģ dehydratase (arpl) 427 91 15 15 22 linear in conidial gene, PLN 12-NOV-1999 complete 419 143 359 123 299 103 239 83 179 120 46 60

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                   LysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp
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                                                                                                                                                                                                                                                                                  IleThrPheSerAspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyr
                                                              ATCGGACTGCGAAAGTGGGATGACATGCCTGCGGAAGACTACATGGCCATGATTTCTGAC
                                                                                          PheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer
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ATGGACTTCTTGGGTGACCCCACCGTCAAGACCCAGCATCTGCTGGGCGAGTCCTGGTGG
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join(331. .370,419. .474,529. .9
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/gene="arp1"
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strain="B-5233"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="arp1"
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US-10-507-132-2 (1-172) x AY098657 (1-424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6TIZ4, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)
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Sordariomycetidae; Ophiostomatales; Ophiostomataceae;
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                                                                                                                                                              /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIG
MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH
AHSANTHWYRKVDGVWKFA"
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/mol_type="genomic DNA"
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/db_xref="GI:21238824"
                                                                                                                                                                                                                                                                                                             gene="SD"
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:104300"
/country="United Kingdom"
                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/isolate="GR10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysVallleAlaPro

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr
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                                                                                                                                                                                                                                                                                  Direct Submission
Direct Submission
Submitted (22-APR-2002) Wood Science, University of British
Submitted (4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
Location/Qualifiers
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Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostom
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Ophiostoma piceae isolate
partial cds.
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/db_xref="G1:21238830"
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join(<1. .69,128. .>423)
                                                                                                                                            /gene="SD"
join(<1. .69,128. .>423)
/gene="SD"
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                                                                                                                                                                                              country="Canada":1. .>423
                                                                                              gene="SD"
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                                                                             Submitted (22-APR-2002) Wood Science, University Columbia, 4th Floor, 2424 Main Mall, Vancouver, Location/Qualifiers
                                                                                                                                                                                                                                                                      Ceratocystis pinicola
Ceratocystis pinicola
Ceratocystis pinicola
Eukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
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Ceratocystis pinicola scytalone
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AY098654.1
                                                                                                                               Direct Submission
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                  /organism="Ceratocystis pinicola"
/mol_type="genomic DNA"
/isolate="0901"
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    _xref="taxon:72031"
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        Ophiostoma minus
Ophiostoma minus
Ophiostoma minus
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiosto
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Fleet,
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Ophiostoma minus isolate
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join(<1...69,138...>432)
/gene="SD"
/codon_start=1
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/db_xref="GI:21238818"
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and Breuil, C
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MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
AHSANKHWYKKVDGVWKFA"
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                                                                          CACCAGCTGCGCGTCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTGGCCGTC
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AAGGGCCACGCACACTCGGCCAACCAGCACTGGTACCGCAAGGTCGACGGCGTCTGGAAG
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MISDPSVLGNPLLRTQHSFGASRWGRVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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/product="scytalone_dehydratase"
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/db_xref="GI:21238828"
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                                                                                                   121 AACAGATC-GATTACCGGTCGTTTCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGAG
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                98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-APR-2002) Wood Science, Columbia, 4th Floor, 2424 Main Mall, Location/Qualifiers
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma
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PhelleGlyGlyThrArgTrpGluLysValSerGluAspGluVallleGlyTyrHisGln
                                                                      PheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHis
                                                                                                                       ---ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGlu
                                                                                                                                                                                         ThrLeu---
                                                                                                                                                                                                                   GAGTGGGCGGACAGGTACGACTCTAAGGACTGGGACCGCCTGCGCAAGTGCATTGCCCCG
                                           (bases 1 to 421)
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MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Ophiostoma piceae"
/mol_type="genomic DNA"
/isoTate="W5"
                                                                                                                                                                                                                                                                                                                                                                                                                                        AHSANQHWYRKVDGVWKFAG"
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/product="scytalone_dehydratase"
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/db_xref="GI:21238832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="scytalone dehydratase"
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/gene="SD"
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Query Match:
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Hypocreomycetidae; Microascales; Microascales
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AY098655.1
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Fleet, C. and Breuil, C.
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                                                      GAGTGGGCGGACAGGTATGACAGCAAGGATTGGGACCGTCTGNGTCGTACCATTGCCCCA
                                                                        GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro
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ACACTAAGAGTGAGCATCTCTCGCTGATATAGCAGAATATATCTTAGTTCTTACTAACAA 120
                         ThrLeu-----
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MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
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                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                             'gene="SD"
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Ophiostoma piliferum isolate
gene, partial cds.
AY098663
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Ophiostoma piliferum
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Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, (
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiosto
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                                                                                                   /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGH
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                                                                                                                                 /Codon_start=1
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/protein_id="AAM34809.1"
/db_xref="GI:21238836"
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join(<1...69,119...>414)
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2 (bases 1 to 414)
Fleet, C. and Breuil, C.
                                                                                                                                                                                                                                                                                                                                                                                                            Ophiostoma piliferum
Ophiostoma piliferum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                                                                                         Submitted (22-APR-2002) Wood Science, University Columbia, 4th Floor, 2424 Main Mall, Vancouver,
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No.	Score	Query Match Length		B	ID	Description
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N	97	56.4	172	7	ADC16591	
ω	7	4.1	98	4	AAG98943	
44	7	4.1	132	ហ	ABP02041	Abp02041 Human ORF
IJ	7	4.1	187	œ	ADS43113	Ads43113 Bacterial
6	7	4.1	191	10	AEE60274	Aee60274 Cat chlam
7	7	4.1	198	7	ADM04932	Adm04932 Human pro
8	7	4.1	198	9	AEC87862	Aec87862 Human cDN
9	7	4.1	225	8	ADX91359	Adx91359 Plant ful
10	7	4.1	251	7	ABO62543	Abo62543 Klebsiell
11	7	4.1	255	4	AAU21761	Aau21761 Novel hum
12	7	4.1	255	4	AAM83837	Aam83837 Human imm
13	7	4.1	255	7	ADC46402	Adc46402 Human neo
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Query Match

100.0%;

Score 172;

DВ

7;

Length 172;

Sequence 172 AA;

The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the Scytalone dehydrogenase amino acid sequence.

Claim 7; SEQ ID NO 4; 50pp; Japanese.

Gene encoding for scytalone dehydrogenase (SCDH), useful for SCDH inhibitors and evaluating sensitivity to them.

for screening

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N-PSDB; ADC16592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaku K, Watanabe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-2002; 2002JP-00066955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2003; 2003WO-JP001980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scytalone dehydrogenase #SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimizu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
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RESULT 2
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                                                                                                                         Query Match
Best Local S
Matches 97
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                                                                                                                                                                                                                             The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors and evaluating sensitivity to them. The current sequence represents the
                                                                                                                                                                                      Sequence 172 AA;
                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                     Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
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                                                                                                                                                                                                                   Scytalone dehydrogenase amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaku
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                   136 KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172;
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                                                                                                                                         Similarity
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                                                                                LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
                                                           LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
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                                                                                                                       56.4%; So
100.0%; E
tive 0;
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                                                                                                                       Score 97; DB ; Pred. No. 3.1: 0; Mismatches
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                                                                                                                                       DB 7; Le 3.1e-97;
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RESULT 3
AAG98943
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Best Local Similarity
Thes 7; Conserve
RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                               CC PAH84373 to AAH84499 represent Escherichia coli growth and proliferation CC related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth CC and proliferation related proteins given in AA899078 and AA698830 to CAA698999. (I) can be used as potential targets for the generation of new CC antimicrobial agents, and for identification of compounds which interact with the gene products of (I). In addition the expression of (I) and the purification of the proteins, the purified proteins can be used to CC generate reagents and screen small molecule libraries or other candidate CC compound libraries for compounds that can be further developed to yield CC compund libraries for compounds. In addition, nucleic acid probes CC complementary to (I) that are specific for particular species of microorganisms can be used to identify particular microorganism species in clinical specimens, therefore, providing a rapid and dependable method by which to identify the causative agents of a bacterial infection. Also, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for generatic microorganisms that produce such proteins in a species-specific manner. AAH84371 and AAH84670 represent sequencing primers used in the CC used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                        Sequence 98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 476; 522pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-335933/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial infection; microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    screening
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                                                                                            LRIDYRS
                                                                                                                                                        LRIDYRS 52
                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids that inhibit Escherichia coli proliferation, useful for homologous genes and for designing expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0164415P
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                                                                                                                                                              4.1%; 50.
100.0%; Pred. No.
1.00.0%; Mismatches
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ABP02041
ID ABPC
XX
AC ABPC

ABP02041 standard;

protein; 132 AA.

ABP02041;

25-JUN-2002 (first entry)

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The present invention describes substantially purified human proteins (referred to, as open reading frame, ORFX, where X is 1-11491 (see Table 1 CC in the specification). ABN15762 to ABN27752 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated CC disorder in humans, and in the manufacture of a medicament for treating a sequence of a medicament for treating a sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, CC psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders haemorrhage, CC transplantation, cardiovascular diseases, disorders, infectious disease, autoimmune throiditis, myasthenia gravis, graft-versus-host disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host comparative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from comparative disorders, or periodontal disease, and for gut proteins are also compared to the printed specification, but was obtained in electronic format directly from WIPO at fib. wipo.int/pub/published_pct_sequences
                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
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                                                                                                                                                                                                                             Sequence 132
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   37
                                                                               Similarity 7; Conser
RLRKVIA 43
                                                                               Conservative
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                                                               4.1%; 500
100.0%; Pr
                                                                           Score 7; DB;
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0; Mismatches
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                                                                                                              DB 5;
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Query Match

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Length 187;

Sequence 187 AA

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RESULT 5
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                                                                                  Comprising the recombinant DNA construct and method of producing a crop plant control as maize or soybean. The method of producing a transformed plant is a crop plant control as maize or soybean. The method of producing a transformed plant control as maize or soybean. The method of producing a transformed plant control as compared property comprises transforming a plant with the control of property comprises transformed plant, where the control of the recombinant DNA construct is useful for improving plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, contracted to herbicides, extreme osmotic conditions, pathogens or pests, contreased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress composition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not composed plant from USPFO at sequence data for this patent did not composed plant from USPFO at sequence data for this patent did not composed plant growth supposed plant for the printed specification but was obtained in electronic composed plant sequence data for this patent did not composed plant growth sequence content in the sequence data for this patent did not composed plant growth sequence content in the sequence data for this patent did not composed plant growth                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; plant growth regulator; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; into the property of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS43113 standard; protein; 187 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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HINKLE G J.
SLATER S C.
CHEN X.
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                                                                                                                                                     The present sequence is one of a series of outer membrane proteins (ARE60274-ARE60310) derived from cat Chlamydia. The present invention relates to a 1166239 base nucleic acid sequence comprising the genome of cat Chlamydia (AEE60206) or a 7552 base sequence comprising a Chlamydia (AEE602077). Also claimed are cat Chlamydia proteins comprising: inclusion body membrane proteins (AEE60208-AEE60273); outer membrane proteins (AEE60204-AEE60210); type-3 secretion proteins (AEE60311). AEE60310); type-3 secretion proteins (AEE60311); acretins (AEE60310); type-3 secretion proteins (AEE60311). AEE60310); highly antigenic proteins (AEE60339-AEE60339-); heat shock proteins (AEE60313-AEE60393-). AEE60300); and proteins (AEE60335-AEE60392); heat shock proteins (AEE60393-AEE60393-). AEE60011-AEE60393-AEE60392); heat shock proteins (AEE60393-AEE60393-). Probes which target these nucleic acid or protein (AEE60401-AEE60526). Probes which target these nucleic acid or protein (AEE6041-AEE60526). Probes which target these nucleic acid or protein (AEE60312-AEE60310); and proteins which target these nucleic acid or protein (AEE60312-AEE60310); and proteins which target these nucleic acid or protein (AEE60310-AEE60310); and proteins which target these nucleic acid or protein or base sequence determination, where the nucleic acid hybridization or base sequence determination or Southern hybridization process. Such screening methods are useful for detecting conjunctivitis, preumonia and bronchitis, based on the presence or absence of alteration in a gene (presence or absence of deletion or the point mutation). The disclosed sequences are also useful in producing vaccines for provention of chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0%; Matches 7; Conservative
                                                                   Matches
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                                                                                                                     Sequence 191
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 69; 19pp; Japanese.
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                                                                              Local
                                                                                                                                              preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid derived from
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                                                                Similarity 7; Conser
                                        ADSYDSK 33
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               ADSYDSK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                    leic acid derived from cat Chlamydia, useful as probe conjunctivitis, pneumonia or bronchitis.
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                                                                4.1%; Sillarity 100.0%; Conservative 0;
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                                                                                                                                              infection of Chlamydia.
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                                                                Score 7; DB 1; Pred. No. 82; 0; Mismatches
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o. 82;
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Best Local S
Matches 7
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stomach ulcer; gastrointestinal ulcer
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Seki N, Yoshikawa T,
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The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.; Antiulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gast
                                                                                                Human cDNA clone protein NT2NE20159740, SEQ ID 3617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 3617; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuki T, Wakamatsu A, Si
Hio Y, Otsuka K, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 7; DB 7
k; Pred. No. 85;
0; Mismatches
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inflammation; gastritis;
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K, Irie
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RESULT 9
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Best Local :
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                                                                                                                                                                                                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heatbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New full-length cDNA sequences, useful for treating diseases, osteoporosis, cancer, inflammation, gastritis, or gastroduode
  06-MAY-1999;
                                                   28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant full length insert polypeptide seqid 54023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADX91359 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-667421/69.
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12-APR-2002; 2002EP-00008400.
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                                                                                                           19-FEB-2004.
                                                                                                                                                               US2004034888-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel human cDNAs (AEC84246-AEC86688)
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                                                                                                                                                                                                                                                                                              yield; plant growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REAS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity res 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing functions of the proteins, and for developing medicines for diseases osteoporosis, cancer, inflammation, gastritis, or gastroduodenal er. Note: The sequence data for this patent did not form part of the nted specification but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3617; 296pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                              tion; lignin production; plant growth regulator;
plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.1%; Score 7; DB 9
100.0%; Pred. No. 85,
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hio Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T, Wakamatsu A; Sato H, Otsuka K, Nagai K, Irie M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or gastroduodenal ulcer.
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RESULT 10
ABO62543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp. seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cf the invention are also useful in physical arrays of molecules and as improving plant tolerance to cold, heat, drought, herbicides, extreme cosmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring clincreased resistance to plant disease, for producing galactomannan, clincreased resistance to plant growth are provided by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
              29-JAN-1999;
                                            27-JAN-2000; 2000US-00489039
                                                                                                                                     Klebsiella pneumoniae
                                                                                                                                                                                                                   Klebsiella pneumoniae polypeptide seqid 9060
                                                                                                                                                                                                                                                    29-JUL-2004
                                                                                                                                                                                                                                                                                 ABO62543;
                                                                                                                                                                                                                                                                                                                 ABO62543 standard; protein; 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 54023; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                      Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-180133/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-2001; 2001US-00985678
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SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
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                                                                                                                                                                   t expression vector; transcription regulatory element; pneumoniae protein; antibacterial; Vaccine.
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              99US-0117747P
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Pred. No.
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RESULT 11
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XX AAU21
XX AAU21
DT 06-DE
XX Humar
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XW musecu
XW musecu
XW musecu
XW neurc
XX Homo
XX
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Best Local S
Matches 7
    18-APR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
07-JUL-2000
11-JUL-2000
11-JUL-2000
11-JUL-2000
26-JUL-2000
26-JUL-2000
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; ranal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 251
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N-PSDB; ACH96094.
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                             The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders involving neoplastic disease such as hyperproliferative glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, gastrointestinal disorders, muscular disorders such as neural disorders, gastrointestinal disorders, The polymucleotide sequences of the invention are also useful disorders. The polymucleotide sequences of the invention are also useful disorders and polymucleotide sequences of the invention are also useful in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
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activity
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DB; AAS34960.
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in electronic format directly from WIPO at
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Pred. No.
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RESULT 13
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                                                                                                                                                                                                                                                                            AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 capresent sequences used in the exemplification of the present invention.
                                                                                                                                                                             Query Match 4.1%; Score 7; Best Local Similarity 100.0%; Pred. No. Matches 7; Conservative 0; Mismatcl
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                                                                                                                                                                                                                                                   Sequence 255 AA;
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N-PSDB; AAK56618.
                               ADC46402 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11;
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05-JAN-2001;
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RESULT 14
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ID ADX79
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AC ADX79
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17-NOV-2000;
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01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising the nucleic acid (expressing the protein), an isolated antibody that binds specifically to the isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the polypeptide, identifying an activity in a biological assay, and the gene corresponding to the cDNA sequence. The polypeptides, polynucleotides and antibodies are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as hyperproliferative diseases or cancer, autolumnune disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematologic disorders (e.g. anaemia or thrombocytopaenia), allergic reactions including asthma or eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences (including their domains, epitopes, full-length proteins, allelic variand or species homologues). Also included are there encoding nucleic acids, recombinant vector comprising the nucleic acid, a recombinant host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human neoplastic disease-associated polypeptides and polynucleotides, useful for diagnosing, preventing, prognosticating or treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000;
08-DEC-2000;
         plant protectant; plant growth regulant; gene therapy; plant;
                                                                Plant full length insert polypeptide segid 49108
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21-APR-2005
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2000US-0251479P.
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2000US-0249299P
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Pred. No.
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o. 1.1e+02;
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ADO02033 ID ADOO XX

ADO02033 standard; protein; 258 AA

RESULT 15

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cc polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for comotic conditations, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for moducing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                       Query Match
Best Local S
Matches 7
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                                                                                                                                                                                                                  Sequence 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathogs pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1999;
05-NOV-2001;
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                                                                                                                                                                                                                                                                            Revised record issued
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115
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SCREEN S E.
TABASKA J E.
CAO Y.
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ZHOU Y.
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Conservative 0;
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2001US-00985678.
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100.0%; Pred. No. 1.
ive 0; Mismatches
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hes 0;
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22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
22-MAR-2000;
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17-FEB-2000;
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                                                           Pilgrim
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(KEDD/
(YUGG/
(JIAN/
                                                                                                                                                                                                                                                                                                              09-AUG
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(FROM/)
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                         2004-225755/21.
DB; ADO02032.
                                                T J,
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SAMAHA R S.
PILGRIM M L.
CREELMAN R A.
DUBELL A N.
RATCLIFFE O.
KUMIMOTO R.
SHERMAN B K.
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REUBER T L.
KEDDIE J S.
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HEARD J E.
RIECHMANN J
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BROUN P E
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                                                            Fromm ME, H
Reuber TL,
IL, Creelman
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2001US-00837444.
2002US-00958131.
2002US-00171468.
2002US-00225066.
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2000US-00533648.
2000WO-US009448.
2000US-00713994.
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2000US-00506720.
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                                                           Heard JE, Riechn
, Keddie JS, Yu
an RA, Dubell AN,
                                                           Riechmann JL, Ac
S, Yu G, Jiang C
ll AN, Ratcliffe
                                                                             Adam LJ,
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                                                           m LJ, Broun PE;
Samaha RS;
, Kumimoto R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eaf morphology;
shade avoidance
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Claim
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                                    SEQ ID NO 446; 213pp; English.
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The invention relates to a transgenic plant comprises a recombinant polynucleotide having a sequence or its complementary exquence comprising a sequence encoding a polypeptide, that initiates transcription (i.e. a transcription factor) from Arabidopsis, Soybean, Rice, Rape or Corn, comprising any of the sequences appearing as AD00158 constitutive, inducible or tissue-specific promoters and a recombinant complynucleotide described above), a bost cell comprising a transgenic plant to grow a progeny plant, an expression cassette (comprising a factor that is modulated by or interacts with a polypeptide encoded by the polypucleotide sequence and identifying a transgenic plant plant is useful for producing a modified plant having a modified trait, identifying a factor that is subject to a regulatory effect of any of the polypucleotide sequence that is subject to a regulatory effect of any of the polypucleotide sequence that is subject to a regulatory effect of any of the polypucleotide sequence to calcidate to the polypucleotide sequence to the polypucleotide sequence to desire to be polypucleotide sequence to calcidate the polypucleotide sequence to polypucleotide to expression of continuity, reduced sensitivity to abscrize interact, tolerance to salt, an altered succeptibility to polypucleotide sequence to early the polypucleotide sequence to early the polypucleotide secuence to the p sterols, upregulation of genes involved in secondary metabolism, incrin root anthocyanins, increase in plant anthocyanins, and alteration light response or shade avoidance. The present sequence represents a thalecress transcription factor of the invention. increase ä

Sequence 258 AA;

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Matches
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188
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                              Conservative
194
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                            Score 7; DB 8; Pred. No. 1.1
0; Mismatches
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Search completed: December time : secs 5 2006, 01:07:51

New transgenic plant, useful in developing improved characteristics or traits.

phenotypes with altered

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Result
No.
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Maximum
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| /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
| /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
| /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
| /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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US-08-658-335B-30
US-08-658-335B-30
US-09-319-806-4
US-09-902-540-12543
US-09-230-337-31
US-09-270-767-42397
US-10-104-047-2880
US-09-155-770-7
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US-09-155-770-7
US-09-155-770-7
US-09-481-206-4
US-08-687-379-6
US-08-687-379-6
US-08-687-379-8
US-08-483-327-2
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Sequence 4, Appli
Sequence 12543, A
Sequence 31, Appl
Sequence 42397, A
Sequence 42397, A
Sequence 7
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Sequence 9060, Ap
Sequence 30, Appl
Sequence 30, Appl
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US-08-971-982-39	US-08-777-192-39	US-08-377-687-39	US-08-448-481-5	US-08-640-847C-36	US-10-115-123-305	US-10-012-542-305	US-09-461-325-305	US-09-949-016-11209	US-09-945-901-58	US-10-007-747-58	US-10-038-937-58	US-09-386-123-58	US-09-648-797-58	US-08-935-105A-58	US-08-940-035A-58	US-08-940-086A-58	US-08-486-273A-58	US-08-231-193A-58
Sequence :	Sequence :	Sequence :	Sequence !	Sequence :	Sequence :	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence !	Sequence!	Sequence!	Sequence!	Sequence !	Sequence !
39, Appl	39, Appl	39, Appl	5, Appli	36, Appl	305, App	305, App	305, App	11209, A	58, Appl	•	58, Appl	58, Appl	58, Appl	•	58, Appl	58, Appl	58, Appl	58, Appl

ALIGNMENTS

APPLICANT: Homburger et al. FITTLE OF INVENTION: Nucleic acids and proteins of FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 56503 LENGTH: 64 TYPE: PRT Sequence 41287, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION: APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094 CURRENT APPLICATION NUMBER: US/09/270,767 CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 62517 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 41287 US-09-270-767-56503; Sequence 56503, Application US/09270767; Patent No. 6703491 ; ORGANISM: Drosophila melanogaster US-09-270-767-56503 밁 S ; ORGANISM: Drosophila melanogaster US-09-270-767-41287 US-09-270-767-41287 RESULT 1 Query Match Best Local S Matches GENERAL INFORMATION: Best Local Query Match TYPE: PRT LENGTH: 64 35 YRSFLDK 41 50 YRSFLDK 56 l Similarity 7; Conserve 7; Similarity Conservative 4.1%; Score 7; 100.0%; Pred. No. 4.1%; Score 7; 100.0%; Pred. No. 0 Mismatches DB 2; . DB . 22 22 of Drosophila melanogaster Length 64; Length 64; 0; Indels 0 Gaps 0

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US-09-711-164-413
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   ; Sequence 30, Application in the control of the co
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SEQ ID NO 9060
LENGTH: 251
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 100.0%;
Matches 7; Conservative (
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Best Local
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APPLICANT: Gary Br
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APPLICANT: Forsyth
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
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ORGANISM: Escherichia coli
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Ohlsen, Kari
                                                                                                                                                                           Application US/08629291A
Coruzzi, Gloria
Oliveira, Igor
Lam, Hon-Ming
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00.0%; Pred. No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 259 amin-
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Patent No. 5
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Best Local Similarity
Matches 7; Conserv
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                                         ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/658,335B
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NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                     APPLICANT: Hsieh, M. TITLE OF INVENTION: NUMBER OF SEQUENCES:
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TITLE OF INVENTION: PLANT GLI
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 08-APR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: siz
                             FILING DATE:
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TELEFAX: (212) 869-9741/8864
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                CLASSIFICATION:
                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                           STATE:
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Oliveira, Igor
Lam, Hon-Ming
Heileh, Ming-Heilun
VENTION: PLANT GLUTAMATE RECEPTORS
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                             05-JUN-1996
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100.0%; Pred. No. 32
tive 0; Mismatches
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GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
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4.1%; Score 7; DB
Local Similarity 100.0%; Pred. No. 32
hes 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-082
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Coruzzi, Gloria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 FEDGRET 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 FEDGRET 54
                                                                                                                                             LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/406,640 FILING DATE: 27-Sep-1999 CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                TELEFAX: (212)
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   Conservative
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Lam, Hon-Ming
 4.1%; Score 7; DB;
100.0%; Pred. No. 32
tive 0; Mismatches
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                     DB 2;
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                                      Length 259;
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PRIOR FILING DATE: 2000-07-10
PRIOR OF SEQ ID NOS: 16825
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US-09-319-806-4
                                                                                                                                                                    US-09-902-540-12543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-902-540-12543
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SEQ ID NO 4
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Crameri, Reto
APPLICANT: Hemman, Stefanie
APPLICANT: Blaser, Kurt
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
TITLE OF INVENTION: Aspergillosis
                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: MYXCOCCUS xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12543, Application US/09902540 Patent No. 6833447
                                                                                               Matches
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Best Local :
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                                                                                                                Best
                                                                                                                                Query Match
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: SE9604815-2
PRIOR FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: PCT/SE97/02171
PRIOR FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                    ORGANISM: Myxococcus xanthus
                                                                                                                Local
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                       232 PTLRIDY 238
                                                        44 PTLRIDY 50
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7; Conserva
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7; Conserv
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                                                                                           4.1%; Score 7; DB 2 llarity 100.0%; Pred. No. 36; Conservative 0; Mismatches
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100.0%; Pred. No. 36;
rative 0; Mismatches
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o. 36;
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Gaps

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Length 286 Indels

Length 287;

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Indels

0,

Gaps

RESULT 10 US-09-230-637-31

Application US/09230637

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RESULT 11

US-09-270-767-42397
; Sequence 42397, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
   APPLICANT: Homburger et al.
   TITLE OF INVENTION: uncleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; NUMBER OF SEQ ID NOS: 62517
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US-10-104-047-2880
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Best Local Similarity
'Arches 7; Conserva
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                Sequence 2880, Application US/10104047
PATENT NO. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42397
LENGTH: 361
TYPE: PRT
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Best Local :
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SEQ ID NO 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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CURRENT APPLICATION NUMBER: US/09/230,637
CURRENT FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/022,591
PRIOR FILING DATE: 1996-07-25
PRIOR APPLICATION NUMBER: PCT US 97/1293:
PRIOR APPLICATION NUMBER: PCT US 97/1293:
PRIOR FILING DATE: 1997-07-24
NUMBER: PCT US PRIOR FILING DATE: 1997-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hayward, Gary
APPLICANT: Nicholas, John
APPLICANT: Hardwick, J. Marie
APPLICANT: Reitz, Marvin
TITLE OF INVENTION: No. 6264958el Genes of
TITLE OF INVENTION: Associated Herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 294
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                                                                                                                                                                                                                                          270 RSFLDKL 276
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                                                                                                                                                                                                                                                                                                                    Conservative
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1996-07-25
TIMBER: PCT US 97/12931
                                                                                                                                                                                                                                                                                                                                         100.0%;
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L00.0%; Pred. No. 44;
ive 0; Mismatches
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; LENGTH: 626
; TYPE: PRT
; ORGANISM: Homo s
US-09-155-770-7
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Best Local Similarity
"hes 7; Conserva
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2880
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                                                   ; ORGANISM: Human
US-09-949-016-8753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA ENCODING DP-75 AND A PROCESS FOR ITS FILE REFERENCE: 200130.418
CURRENT APPLICATION UNMEER: US/09/155,770A
CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.:
SEQ ID NO 2880
                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8753
LENGTH: 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Duhl, Da
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                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 7; Conservative
                  Query Match
                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER: OF SEQ ID NOS: 207012
NUMBER: OF SEQ ID NOS: 207012
Best Local Similarity
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100.0%; Pr
4.1%;
100.0%;
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%; Pred. No. 72;
0; Mismatches
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Score 7; D
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 DB 2;
                Length 806;
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GENERAL INFORMATION:

APPLICANT: Heinemann Ph.D., James R.

APPLICANT: Hollmann Ph.D., Michael Nan

APPLICANT: Hollmann Ph.D., Jan E.

ITITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 So. Flower St., Suite 2000

CITY: Los Angeles

STATE: California

COUNTRY: United States

ZIP: 90071-2921

COMPUTER: JEM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/07/718,575

FILING DATE: 19910813

CLASSIFICATION NUMBER: 31192

REGISTRATION NUMBER: 31192

REGISTRATION NUMBER: 31192

REGISTRATION NUMBER: 31192

REGISTRATION NUMBER: 31192

REFERENCE/DOCKET NUMBER: 318962

TELECOMMUNICATION INFORMATION:

MAME: Reiter Ph.D., Stephen E.

REGISTRATION NUMBER: 31192

REFERENCE/DOCKET NUMBER: 31192

REGISTRATION NUMBER: 31192

REGISTRATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 883 amnio acids

TYPE: AMINO ACID

TOPOLOSY: linear

HOLECULE TYPE: protein

US-07-718-575-4
Search completed: December Job time : 55 secs
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US-07-718-575-4
                                                                                                                                                                  Query Match 4.1%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 98; Matches 7; Conservative 0; Mismatches
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Patent No. 5202257
GENERAL INFORMATION:
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                                                                                                                         162 FEDGRET 168
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                                                                                   FEDGRET 583
                   5, 2006, 01:14:43
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Maximum DB
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seq length: 2000000000
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172
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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                             US-10-425-115-186523

US-10-287-274-413

US-10-287-274-413

US-10-287-274-459

US-10-369-493-21543

US-10-425-115-33577

US-10-425-115-33577

US-10-425-115-32523

US-10-425-113-488

US-10-425-114-49108

US-10-425-114-49108

US-10-425-114-49108

US-10-425-114-49108

US-10-425-114-49108

US-10-425-114-49108

US-10-412-6998-446

US-10-612-358-4

US-10-612-358-4

US-10-424-599-209185

US-10-424-599-209185

US-10-424-599-209185

US-10-506-454-684

US-10-97-64-864-804

US-10-104-047-2880

US-11-079-463-7267
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3617, Ap
335717,
54023, A
167826,
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187642,
               68, Appl
7267, Ap
51224, A
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488, Aj
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APPLICANT: LA ROSA, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 186523

LENGTH: 75

TYPE: PRT
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7 4.1 533 4 US-10-437-963-108161 7 4.1 620 5 US-10-310-671-7 7 4.1 626 4 US-10-310-671-7 7 4.1 626 4 US-10-310-671-11 7 4.1 716 4 US-10-310-313-334 7 4.1 719 4 US-10-313-334 7 4.1 750 4 US-10-37-963-185546 7 4.1 750 4 US-10-479-963-185546 7 4.1 807 4 US-10-478-245-7 7 4.1 807 4 US-10-367-094-185 7 4.1 883 4 US-10-367-094-183 7 4.1 883 5 US-10-958-626-141	4 5	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29
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4 US-10-437-963-108161 5 US-10-450-763-38123 4 US-10-310-671-17 4 US-10-310-671-11 5 US-10-30-671-11 6 US-10-30-673-334 6 US-10-103-313-334 7 US-10-437-963-185546 7 US-10-437-963-185546 7 US-10-437-963-185546 7 US-10-478-245-7 8 US-10-367-094-183 9 US-10-368-661-141	883	883	883	883	883	877	875	847	807	762	750	719	716	626	626	600	533
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	141, App	141, App	102, App	•	190, App	183, App	178, App	Appli	185, App	10509, A	185546,	334, App	12942, A	11, Appl	7, Appli	38123, A	108161,

ALIGNMENTS

and

Other Molecules

Associated

With

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US-10-287-274-413
Sequence 413, Application US/10287274
Publication No. US20030181408A1
GENERAL INFORMATION:
APPLICANT: FOrByth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLS OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
FILE REFERENCE: ELITRA, ODSDV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 09/711164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-115-186523
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Clone
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vative 0; Mismatches
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100.0%; Pred. No.
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Sequence 21543, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-413
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US-10-424-599-187642
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APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION OUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 187642

LENGTH: 139
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                   NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21543
LENGTH: 187
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                                                                                             TITLE OF INVENTION: EXERESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
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LOCATION: (1)..(139)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                TYPE: PRT
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ORGANISM: Methanobacterium thermoautotrophicum
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FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 3617
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-3617
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                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_6927C.1.pep US-10-425-115-335717
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                                                                                                                                                                                                                        APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335717
LENGTH: 219
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Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH OF INSTITUTE OF INVENTION: No. US20040005560A1e1 full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.1%; Score 7; DB Best Local Similarity 100.0%; Pred. No. 1. Matches 7; Conservative 0; Mismatches
                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local
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                                                                                                                                                                                                                 TYPE: PRT
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7; Conserva
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Similarity 100.0%;
7; Conservative (
GSQVQKS
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 85
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                                                                      Score 7; DB 4; Pred. No. 1.2
0; Mismatches
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o. 1.2e+02;
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o. 1.1e+02;
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RESULT 7 US-10-425-114-54023 ; Sequence 54023, Application US/10425114

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Query Match
Best Local Similarity
7; Conserve
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US-10-425-114-54023
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SEQ ID NO 54023
LENGTH: 225
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SEQ ID NO 167826
LENGTH: 228
                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
FILE REFERENCE: 38-21 (53223) B
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APPLICANT:
APPLICANT:
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                                APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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CURRENT FILING DATE: 2003-04-28
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                  APPLICANT:
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CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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     Zhou, Yime
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Screen, Steven E
Tabaska, Jack E
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Pred. No.
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Pred. No. 1.2e+02;
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o. 1.3e+02;
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US-10-425-114-49108

Sequence 49108, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:

APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua

Zhou, Yihua Kovalic, David I Screen, Steven J

APPLICANT:

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; OTHER INFORMATION: Clone ID: MRT4577_143745C.1.pep US-10-425-115-232623
                                                                                                                           ; OTHER INFORMATION: Xaa equals any of the naturally occurring US-10-103-313-488
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                                                                                                                                                                                                                                                                                                                                                  Prior Application removed - See File Wrapper or Palm SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 232623
LENGTH: 236
                                                             Matches
                                                                           Query Match
Best Local
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Best Local (
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OTHER INFORMATION: Xaa e NAME/KEY: misc feature LOCATION: (223)

OTHER INFORMATION: Xaa e NAME/KEY: misc feature LOCATION: (232)
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
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CURRENT FILING DATE: 2003-04-28
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FILE REFERENCE: 38-21(53222)B
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LOCATION: (1)..(236)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                     LENGTH: 255
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116 DRLRKVI 122
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                     36 DRLRKVI 42
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                                                          Similarity 7; Conserv
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Pred. No.
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SEQ ID NO 49108
LENGTH: 255
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
FOTHER INFORMATION: Clone ID: 70
                                                                             CURRENT APPLICATION NUMBER: US/10/412,699B
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR APPLICATION NUMBER: 09/533,029
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,648
PRIOR APPLICATION NUMBER: 09/533,648
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Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ratcliffe, Oliver
APPLICANT: Kumimoto, Roderick
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MBI-0048CIP
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, James
APPLICANT: Fromm, Michael E.
APPLICANT: Heard, Jacqueline E.
APPLICANT: Riechmann, Jose Luis
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              APPLICATION NUMBER: 09/533,648
FILING DATE: 2000-03-22
APPLICATION NUMBER: 09/713,994
FILING DATE: 2000-11-16
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Jiang, Cai-Zhong
Samaha, Raymond R.
Pilgrim, Marsha L.
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Reuber, T. Lynne
Keddie, James S.
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DuBell, Arnold N.
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D. US20040045049A1
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NUMBER: 09/819,142
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Pred. No. 1.4e+02;
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; MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 30: US-10-223-047-30
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US-10-223-047-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data
NUMBER OF SEQ ID NOS: 2011
SOFTWARE: PatentIn version 3.2
SEQ ID NO 446
LENGTH: 258
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                    Query Match
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TYPE: PRT
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                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 7; 1 Local Similarity 100.0%; Pred. No. 108 7; Conservative 0. Minutes
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/406,640
FILING DATE: 27-Sep-1999
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heieh, Ming-Heiun
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
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Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/223,047 FILING DATE: 16-Aug-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                          STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1155 Avenue of the Americas
                                                                                                                                                                             LENGTH: 259 amino acids
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   ilarity 100.0%; | Conservative 0;
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Lam, Hon-Ming
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   ; Score 7; DB 4
%; Pred. No. 1.4
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5. 1.4e+02;
                    DB 4; Ler
5. 1.4e+02;
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                                     Length 259
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Sequence 11818, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatear, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 11818
LENGTH: 293
TYPE: PRI
TOTAL AND THE PRIOR OF T
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APPLICANT: Hemman, Stefanie
APPLICANT: Hemman, Stefanie
APPLICANT: Blaser, Kurt
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
TITLE OF INVENTION: Aspergillosis
CURRENT APPLICATION UNUMBER: US/10/612,358
CURRENT FILING DATE: 1906-12-20
PRIOR APPLICATION NUMBER: E3904815-2
PRIOR APPLICATION NUMBER: PCT/SE97/02171
PRIOR APPLICATION NUMBER: PCT/SE97/02171
PRIOR APPLICATION NUMBER: US/9/319806
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: US/9/319806
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEO ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
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US-10-612-358-4
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; Sequence 4, Application US/10612358
; Publication No. US20050074410A1
; GENERAL INFORMATION:
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US-10-369-493-11818
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LENGTH: 286
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                          Y Match 4.1%; Score 7; DB 4; Length 293;
Local Similarity 100.0%; Pred. No. 1.6e+02;
hes 7; Conservative 0; Mismatches 0; Indels
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Db 218 DRLRKVI 224

Search completed: December 5, 2006, 01:17:56
Job time : 188 secs

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US-11-056-355B-52964
US-11-056-355B-81939
US-11-056-355B-81939
US-11-056-355B-52963
US-11-056-355B-52963
US-11-056-355B-52963
US-11-056-355B-52963
US-11-056-355B-59499
US-11-174-307B-4610
US-11-330-449-902-31790
US-11-330-403-5226
US-11-330-403-5226
US-11-330-403-52140
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- 2006 Biocceleration Ltd
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Sequence 3617, Ap
Sequence 76, Appl
Sequence 81940, A
Sequence 17570, A
Sequence 52964, A
Sequence 81939, A
Sequence 17569, A
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41	18	988	937	937	889	887	884	883	883	883	879	833	833	832	832	. 817	817	765	113
7	σ	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	-
US-11-434-137-2676	US-10-520-521-8	US-11-056-355B-79945	US-11-056-355B-92674	US-11-056-355B-88918	US-11-221-332-100	US-11-056-355B-76256	US-11-056-355B-79946	US-11-248-718-141	US-11-226-554-141	US-11-056-355B-79947	US-11-056-355B-76257	US-11-056-355B-92675	US-11-056-355B-88919	US-11-056-355B-92676	US-11-056-355B-88920	US-11-056-355B-87049	US-11-056-355B-76258	US-11-330-403-12624	US-TT-056-355B-8/050
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
2676, Ap	8, Appli	79945, A	92674, A	88918, A	100, App	76256, A	79946, A	141, App	141, App	79947, A	76257, A	92675, A	88919, A	92676, A	88920, A	87049, A	76258, A	12624, A	0/050, A

ALIGNMENTS

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; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pyricularia oryzae
US-10-507-132-4
                                                                                                                                                                                        US-10-507-132-2
Sequence 2, Application US/10507132
Publication No. US20060223136A1
GENERAL INFORMATION:
APPLICANT: Kolchiro KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1554-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10507132

Publication No. US20060223136A1
GENERAL INFORMATION:
APPLICANT: Koichiro KAKU et al.
TITLE OF INVENTION: AGENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGENCULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/507,1:
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                       121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
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                                                                                                                                                                                                                                                                                                                                                                                                               61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Pred. No. 9.2e-178;
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                                                                           RESISTANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-507-132-19
             APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVE1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                               US-11-293-697-3617
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Publication No. US20060223136A1
GENERAL INFORMATION:
APPLICANT: KO1Chiro KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT PILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR APPLICATION NUMBER: JP 2002-6955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 33
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SEQ ID NO 2
LENGTH: 172
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Best Local Similarity 100.0%;
                                                                                                                                                                                                            Sequence 3617, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
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Best Local Similarity
SEQ ID NO 3617
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PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide derived fro OTHER INFORMATION: Pyricularia oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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100.0%; Pr
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0; Mismatches
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Pred. No.
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lo. 0.022;
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; TYPE: PRT
; ORGANISM: Homo
US-11-293-697-3617
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                                                                                              ; FEATURE:
, NAME/KEY: peptide
; LOCATION: (1)..(258)
; OTHER INFORMATION: Ceres Seq. ID
US-11-056-355B-81940
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Best Local Similarity
Thehes 7; Conservat
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APPLICANT: SHARMA, SHASHI B.
APPLICANT: SHARMA, SHASHI B.
TITLE OF INVENTION: GENETIC MANIPULATION OF CO.
FILE REFERENCE: NBLEG42:US
CURRENT APPLICATION NUMBER: US/11/179,064B
CURRENT FILING DATE: 2005-07-11
PRIOR PELICATION NUMBER: 60/587,020
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 79
NUMBER OF SEQ ID NOS: 79
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                                                                                                                                                                                                           TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT PLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 81940
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 76, Application US/111
Publication No. US20060123508A1
GENERAL INFORMATION:
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                                  Matches
                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                               TYPE: prt
ORGANISM: Arabidopsis thaliana
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                                                  Similarity
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100.0%; Pred. No.
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                                                               Length 258
                                    Indels
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US-10-953-349-17570

Sequence 17570, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Best Local Similarity
7; Conservat
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US-11-056-355B-81939
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Sequence 81939, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION: APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 52964

LENGTH: 264
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 17570
LENGTH: 264
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                                                                                                                                                                                                                                                                                                                                              NAME/KEY: peptide
LOCATION: (1)..(264)
OTHER INFORMATION: Ceres Seq. ID no. 14304596
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: prt
ORGANISM: Glycine max
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stive 0;
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%; Pred. No. 20;
0; Mismatches
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; Pred. No.
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Sequence 4558, Application US/11174307B

Publication No. US20060143729A1

GENERAL IMFORMATION:

APPLICANT: ALEXANDROV, Nickolai

APPLICANT: BROVER, Vyacheslav

ITILE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY

TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS

FILE REFERENCE: 2750-1601PUS2

CURRENT APPLICATION NUMBER: US/11/174,307B

CURRENT FILING DATE: 2005-06-30

PRIOR APPLICATION NUMBER: 60/583,671

PRIOR APPLICATION NUMBER: 60/583,781

PRIOR APPLICATION NUMBER: 60/583,781

PRIOR FILING DATE: 2004-06-30

PRIOR FILING DATE: 2004-06-30

PRIOR APPLICATION NUMBER: 60/583,651

PRIOR APPLICATION NUMBER: 60/583,651

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US-11-174-307B-4558
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US-10-953-349-17569
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 17569
LENGTH: 280
TYPE: PRT
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LENGTH: 279
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NAME/KEY: peptide
LOCATION: (1)..(279)
OTHER INFORMATION: Ceres Seq. ID no. 12662412
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ORGANISM: Arabidopsis thaliana
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00.0%; Pred. No.
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; NAME/KEY: peptide
; LCCATION: (1)..(280)
; OTHER INFORMATION: Ceres
US-11-056-355B-52963
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US-11-056-355B-52963
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
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SEQ ID NO 4558
LENGTH: 280
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SEQ ID NO 52963
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CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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OTHER INFORMATION: >g1|50252562|dbj|EAD28735.1| WRKY family transcription factor-lik OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)]
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OTHER INFORMATION:
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                                                                                                              TYPE: prt
ORGANISM: Glycine max
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NAME/KEY: misc_feature
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OTHER INFORMATION: PFam Name: WRKY; PFam
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ORGANISM: Glycine max
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7; Conservative 0;
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                       Seq.
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Pred. No.
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; NAME/KEY: peptide
; LOCATION: (1)..(292)
; OTHER INFORMATION: Ceres
US-11-056-355B-52962
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Matches 7
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Best Local S
Matches 7
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Publication No. US20066107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOUTWARE: Patentin version 3.3
SEQ ID NO 17568
LENGTH: 292
                                                          Query Match
Best Local S
Matches 7
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PRIOR APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 52962
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 52962, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Sequence Determined DNA Fragments and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
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ORGANISM: Glycine
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RESULT 15 US-10-953-349-16815

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Sequence 18815, psplication BS/10953349

Philication And INSCRIPTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DT STORY DATE OF THE PROPERTY APPLICATION AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DETERMINED DATE OF THE PROPERTY APPLICATION AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DETERMINED DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

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TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

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TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

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TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: SEQUENCE DATE OF THE PROPERTY AND CORRESPONDING POLYPEPTIONS

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Maximum DB seq length: 2000000000
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ALIGNMENTS

A; Molecule type: DNA

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                                                                                                                                                                                                                                                               C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004 C;Accession: C65058 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I.R.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: linear chromosom.
C;Superfamily: nitrilase (carbon-nitrogen hydrolase)
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A;Residues: 1-290 <KUR>
A;Cross-references: UNIPROT:Q8UA64; UNIPARC:UPI0000D2221; GB:AE007870; PIDN:AAK89885.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98295
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C; Accession: C98295
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A; Status: preliminary; nucleic acid
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                                                                                                                                                A; Experimental C; Superfamily:
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A.; Liu, F.; Wollam, C.; Allinger, M.;
                                                                                                                                                                                                                                                                                                                                                                                      ;Species: Escherichia coli
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;Map position: linear chromosome
                                                                                             Query Match
Best Local
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Experimental source: strain K-12, substrain MG1655
Superfamily: ferredoxin-like protein, FixX type
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                                                                                                                                                                                                                                 sequence not shown;
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hypothetical protein wbfE otnD [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Pate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004 C;Accession: S70957, T44317 C;Accession: S70957, T44317 R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R. Mol. Microbiol. 20, 799-811, 1996
                                                                                                                                           RESULT 7
S70957
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C;Genetics:
A;Genet WIH1876
A;Start codon: GTG
C;Superfamily: spore germination protein C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: A;Reference number: A69000; MUID:98037514; PMID:9371463 A;Accession: A69118
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A;Genome: plasm
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A; Residues: 1-152 < KUR >
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R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimac Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44317
               R;Honess, R.W.; Bodemer, W.; Cameron, K.R.; Niller, H.H.; Fleckenstein, B.; Ranceron, Natl. Acad. Sci. U.S.A. 83, 3604-3608, 1986
A;Title: The A+T-rich genome of Herpesvirus saimiri contains a highly conserved A;Reference number: A26269; MUID:86233282; PMID:3012520
                                                                                       thymidylate synthase (EC 2.1.1.45) - saimiriine herpesvirus 1 c;Species: saimiriine herpesvirus 1 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change C;Accession: A26269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, 'A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; MUID:98337999; PMID:8688087
A;Accession: F64369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
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F64369
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
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A;Experimental source: strain O22
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A; Reference number: A; Accession: A26269
                                                                                                                                                                     SYBEHS
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C;Species: Methanococcus jannaschii
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HTH transcriptional regulator, archaeal type
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R:Krubasik, P.; Sandmann,
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A;Genetic code: SGC3
C;Superfamily: probabl
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A; Residues: 1-385 < KRU>
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A; Residues: 1-309 <GLA>
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A;Molecule type: DNA
A;Residues: 1-294 <HON>
A;Residues: 1-294 <HON>
A;Cross-references: UNIPARC:UPI00001378D3; GB:M13190; NID:g331074;
A;Cross-references: UNIPARC:UPI00001378D3; GB:M13190; NID:g331074;
C;Superfamily: thymidylate synthase; thymidylate synthase homology
C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F;11-294/Domain: thymidylate synthase homology <TDS>
F;176/Active site: Cys #status predicted
                                                                                                                                                                                                   A;Title: A carotenogenic gene cluster from Brevibacterium A;Reference number: Z25303; MUID:20279196; PMID:10821176 A;Accession: T51127
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                                                                                                            A;Cross-references: UNIPROT:Q9KK76; UNIPARC:UPI00000B2FAB; A;Experimental source: DSM 20426; ATCC9175
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A; Residues: 1-573 < KUR>

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C; Date: 13-00 C; Accession: AB1807; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; 111900 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; 111900 R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Tabata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazawa, S.; Sasamoto, S.; Watanabe, A.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazawa, M.; Yamada, M.; Yasuda, M.; Tabata Nakazawa, M.; Yasuda, M.; Yasuda, M.; Tabata Nakazawa, M.; Yasuda, M.; Yasuda, M.; Tabata Nakazawa, M.; Yasuda,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accessio
R;Rieger,
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R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Raja submitted to the EMBL Data Library, August 1999
A;Reference number: Z21563
A;Accession: T34941
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Kolecule type: DNA
A;Residues: 1-528 <SAU>
A;Cross-references: UNIPROT:Q9S2YO; UNIPARC:UPI00000DB2C7; EMBL:AL109663; PI
A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T34941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                 hypothetical protein all4762 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul
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October 1999
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completed: December me : 43 secs

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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64807
                                                                                                                                                                                              A;Description: biogenesis of fimbriae C;Superfamily: outer membrane usher protein C;Keywords: membrane protein E;1-25/Domain: signal sequence #status predi F;26-818/Product: outer membrane usher prote
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C; Function:
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A;Experimental source: strain K-12, substrain MG1655
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 60.0 , Gapext 60.0
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1: uniprot_sprot:*
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       GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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Q80145 glomerella
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Q80116 ophiostoma
Q80111 ophiostoma
Q7x815 bipolaris o
Q2wei4 sordaria ma
Q1434 aspergillus
Q6cnl3 kluyveromyc
Q37866 novosphingo
Q2k386 frizobium m
Q8ua64 agrobacteri
Q7csnl agrobacteri
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Q7csnl agrobacteri
Q6faz4 acinetobact
Q2ua62 aspergillus
Q6faz4 acinetobact
Q2ua62 aspergillus
Q6sfri uncultured
Q2ma62 escherichia
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RAPHY (1.65 ANGSTROMS). ; PubMed=992213; DOI=1 L., Wawrzak Z., Basarab design of potent inhib a water molecule from t 17735-17744 (1998). RAPHY (2.15 ANGSTROMS). ; PubMed=10302670; 1)1097-0134 (19990601)35 alova T., Steffens J.J. rdan D.B.; structures of scytalon lized at physiological 439 (1999).	rystal structure of scytalone dehydra: the rice pathogen, Magnaporthe griss. ructure 2:937-944(1994). RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS). DLINE=98332516; PubMed=965698; DOI-1: kasako M., Motoyama T., Kurahashi Y., kasako M., Motoyama T., Kurahashi Y., kasako M., Motoyama T., rice blast i ytalone dehydratase of a rice blast i hibitor, carpropamid: the structural hibition.", Chemistry, 37.0031.0030/1008)	DLINE=98233280; PubMed=9571787; DLINE=98233280; PubMed=9571787; DNA cloning, expression, and mutagene eded for pathogenicity of the rice blyzae."; Osci. Biotechnol. Biochem. 62:564-566; DLINE=95171111; PubMed=7866745; RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS). DLINE=95171111; PubMed=7866745; andqvist Y.;	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	32 7 4.1 98 1 YGCO ECOLI 33 7 4.1 102 2 Q4ECTB 9RICK 34 7 4.1 114 2 Q4DHW6_TRYCR 35 7 4.1 126 2 Q8QON6 METWA 36 7 4.1 141 2 Q4CT99_TRYCR 37 4.1 141 2 Q4CT99_TRYCR 38 7 4.1 141 2 Q4DPH6_TRYCR 39 7 4.1 143 2 Q9AVM7_9ASTR 39 7 4.1 147 2 Q9DDZ6_CTEOR 40 7 4.1 152 2 Q8YKM8_ANASU 41 7 4.1 177 2 Q9CWD1_MCUSE 42 7 4.1 196 2 Q56657_VIBCH 43 7 4.1 196 2 Q4PG88_USTWA 45 7 4.1 210 2 Q4PG88_USTWA 45 7 4.1 210 2 Q4PG88_USTWA
0.1021/bi981848r; itors of scytalne dehydratase: he active site."; :4<425::AID-PROT6>3.3.CO;2-T; , Basarab G.S., Lundqvist T., e dehydratase-inhibitor pH.";	tase a disease determinant 20."; 0.1021/bi980321b; Yamaguchi I.; Ysis for the complex of ungus and its tight-binding basis of tight-binding	st fungus, Pyricula 1998). 1998).	PRT; 172 AA. niProtKB/Swiss-Prot. 1. 1.94). fungus) (Pyricularia grisea). Pezizomycotina; Sordariomycetes; Magnaporthaceae; Magnaporthe.	Q46905 escherichia Q4ecj8 wolbachia e Q4dhw6 trypanosoma Q4dhw6 trypanosoma Q8q0n6 methanosarc R Q4dph6 trypanosoma Q4dph6 trypanosoma Q4dph6 trypanosoma Q9avm7 chrysanthem Q9avm7 chrysanthem Q9dd26 ctenophorus Q8ykw8 anabaena sp Q9cwd1 mus musculu H Q27904 methanobact Q56657 vibrio chol N Q4pg88 ustilago ma Q4pg88 ustilago ma

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LinkHub; P56221
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAX: Fungal melanin biosynthesis; first step. SUBUNIT: Homotrimer. Each subunit contains an activ in the central part of the hydrophobic core of the functions independently.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Catalyzes two steps in melanin biosynthesis. From scytalone they are two dehydration steps and one reduction steps and one reduction yield melanin.

CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene
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1STD;
2STD;
3STD;
4STD;
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6STD;
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F02982; Scytalone_dh; 1.
PD022193; Scytalone_DH; 1.
                                                                                                                                                                                 Similarity
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D; X-ray; @=1-172.
D; X-ray; @=1-172.
D; X-ray; A/B/C=10-172.
                                                                       VTMKGHAHSANLHWYKKIDGVWKFAGLKDDIRWGEFDFDRIFEDGRETFGDK 172
                                                                                                            MPAEEFVGMVSSKQVLGDPTLRTQHF1GGTRWEKVSEDEV1GYHQLRVPHQRYKDTTMKE
                                                                                                                                              MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA
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172 AA;
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Scytalone dehydratase.
/FTId=PRO_0000097639.
UniProtKB/TrEMBL.
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Pred. No. 5.8e-170;
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SMR; OBNJT7; 1-122.
GO; GO:0016836; F:hydro-lyase activit; GO; GO:0006832; P:melanin metabolism; InterPro; IPR004235; Scytralone_DH.
Pfam; PF02982; Scytralone_dh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002, integrated into U
01-OCT-2002, sequence version
07-FEB-2006, entry version 11.
Scytalone dehydratase (Fragmen
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Ceratocystis pinicola.

Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,

Hypocreomycetidae, Microascales, Microascales incertae sedis,
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
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QBNJI7;
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"Inhibitors and genetic analysis of scytalor
presence of DHN-melanin pathway in sapstain
Mycol. Res. 106:1331-1339(2002).
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                                                                                                     Pfam; PF02982; Scytalone
ProDom; PD022193; Scytalo
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13.4%;

DB 2; Length 122;

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Q9C426 OPHFL
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Q9C426;
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                                                                                                                                 "A scytalone dehydratase gene from Ophiostoma floccosum restores melanization and pathogenicity phenotypes of a melanin-deficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001, sequence version 07-FEB-2006, entry version 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreomycetidae; Microascales; Microascales
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                                                                      Colletotrichum lagenarium mutant.";
Mol. Genet. Genomics 266:126-132(2001)
                                                                                                                                                                                                           MEDLINE=21473268; PubMed=11589570; DOI=10.1007/s004380100534; Wang H.L., Kim S.H., Breuil C.;
                                                                                                                                                                                                                                                                                         STRAIN=387N;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=104300;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; F
Sordariomycetidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ophiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=OSD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scytalone dehydratase
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ProDom; PD022193; Scytalo
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9PEZI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AY214004; AAO60167.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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                                                                                                                                                                                                                                                                                                                                                                                                                               Ascomycota; Pezizomycotina; Sordariomycetes; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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100.0%; Pr
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RESULT 6
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Best Local :
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SMR; Q96426; 22-182.
GO; GO:0016836; F:hydro-lyase activity; IEA.
GO; GO:0016582; P:melanin metabolism; IEA.
GO; GO:0006582; P:melanin metabolism; IEA.
InterPro; IPR004235; Scytalone_DH.
Pfam; PF02982; Scytalone_DH; 1.
ProDom; PD022193; Scytalone_DH; 1.
ProDom; PD022193; Scytalone_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998,
01-NOV-1996,
07-FEB-2006,
 SEQUENCE
                                       Pfam; PF02982; Scytalone_dh; 1.
ProDom; PD022193; Scytalone_DH; 1.
Lyase; Melanin biosynthesis.
                                                                                             EMBL; D86079; BAA13009.1; -; HSSP; P56221; 1IDP. SMR; Q00455; 6-167.
                                                                                                                                                    Copyrighted
Distributed
                                                                                                                                                                                                                                                                                                                      Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.; "Cloning and structural analysis of the melanin biosynthesis gene encoding scytalone dehydratase in Colletotrichum lagenarium."; Appl. Environ. Microbiol. 62:4340-4344(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; micosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glomerella lagenarium (Anthracnose fungus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=SCD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scytalone dehydratase (EC 4.2.1.94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q00455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang H., Breuil C.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=387N;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97111971; PubMed=8953707;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=104
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lagenarium)
                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE
                                                                                                                                                                                                                                                                                           FUNCTION: Catalyzes two steps in melanin biosynthesis. scytalone they are two dehydration steps and one reduct
                                                                                                                                                                                             in the central part of the hydrophobic core of the functions independently (By similarity).
                                                                                                                                                                                                                      H(2)O.

PATHWAY: Fungal melanin biosynthesis; first step.

PATHWAY: Fungal melanin biosynthesis; first step.
                                                                                                                                                                                                                                                              yield melanin.
CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLOLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 YEWADSYDSKDWDRLRK 40
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                                                                                 IPR004235; Scytalone_DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 188
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                    by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry version
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21687
                                                                                                                                                                                                                                                                                                                                                                                                           [GENOMIC DNA].
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  MW.
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Pred. No.
                                                                                                                       Genomic_DNA.
             Scytalone dehydratase.
/FTId=PRO_0000097638.
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8.9e-09;
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Q8NJIO 0
AC Q8NJIO;
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DT 01-0CT-2
DT 07-FEB--
DT 07-FEB--
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                                                 NUCLEOTIDE SEQUENCE.
Fleet C., Breuil C.;
"Inhibitors and genet.
presence of DHN-melan
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QBNJH9
                                   "Inhibitors and genetic analysis of scytalone dehydratase presence of DHN-melanin pathway in sapstain fungi."; Mycol. Res. 106:1331-1339(2002).
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"Inhibitors and genetic analysis of scytalone dehydratase
presence of DHN-melanin pathway in sapstain fungi.";
Mycol. Res. 106:1331-1339(2002).
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Ophiostoma setosum.

Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Pungi; Ascomycota; Ophiostomataceae; Ophiostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002,
01-OCT-2002,
   Copyrighted
Distributed
                                                                                                              Sordariomycetidae;
NCBI_TaxID=38032;
                                                                                                                                    Ophiostoma piliferum.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                               01-OCT-2002, sequence version 1.
                                                                                                                                                                                                Q8NJIO;
01-OCT-2002, integrated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                             Scytalone dehydratase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                      SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0016836; F:hydro-lyase activity; IEA.
GO:0006582; P:melanin metabolism; IEA.
erPro: IPR004235; Scytalone DH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8NJH9; 1-121
                                                                                                                                                                                                                                                                                                                                                                                                                                     PF02982; Scytalone_dh;
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sequence version 1.
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  UniProt Consortium, see http://www.uniprot.org/terms
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                                                                                                                         Ophiostomatales;
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100.0%;
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k; Pred. No. 7.9
0; Mismatches
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Pred. No.
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3. 8.6e-08;
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RESULT 10
QBNIE1 PEZI
QBNIE1 PEZI PRELIMINARY; PRT; 122 AA.

ID QBNIE1;
O1-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-CCT-2002, sequence version 1.
DT 07-PEB-2006, entry version 10.
DE Scytalone dehydratase (Fragment).
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HSSP; P56221; 1LDP.
SMR; OSNUTO; 1-121.
GO; GO:0016836; F:hydro-lyase activity; IEA.
GO; GO:000583; P:metabolism; IEA.
InterPro; IPR00423; Scytalone_DH.
Pfam; PF02982; Scytalone_dh; 1.
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QBNJI5;
01-OCT-2002, integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                              Pfam; PF02982; Scytalone_dh; 1.
ProDom; PD022193; Scytalone_DH; 1.
                                                                                                                                                                                                                                                                         InterPro; IPR004235; Scytalone
Pfam; PF02982; Scytalone_dh; 1.
                                                                                                                                                                                                                                                                                                                                    EMBL; AY098657; AAM34803.1; -; Genomic_DNA.
HSSP; P56221; 1IDP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Fleet C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=104300;
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Sordariomycetidae; Ophiostomat
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GO:0016836; F:hydro-lyase activity; IE
GO:0006582; P:melanin metabolism; IEA.
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121 AA;
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121 AA;
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Pred. No.
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H8_9PEZI
Q8NJH8_9PEZI
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
NCBI_TaxID=61273;
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EMBL; AY09866; AAM34807.1; -; Genomic_DNA.
HSSP; P5221; 11DP.
SMR; QBNIE1; 1-122.
                                                                                                                                                                                   Pfam; PF02982;
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GO; GO:0006582; P:melanin metabolism; IEA.
InterPro; IPR004235; Scytalone_DH.
Pfam; PF02982; Scytalone_dh; 1.
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Fleet C., Breuil C.;
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                                                                                                                                                                                                                              GO:0016836; F:hydro-lyase activity; GO:0006582; P:melanin metabolism; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C., Breuil C.;
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13; Conservative
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                                                                                                                                                         PD022193; Scytalone_DH;
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100.0%; Pred. No. 7.1
ive 0; Mismatches
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QBNJI2;
QBNJI2;
01-OCT-2002, integrated into
                                                                                                                              Pleet C., Breuil C.;
"Inhibitors and genetic analysis of
presence of DHN-melanin pathway in 6
Mycol. Res. 106:1331-1339(2002).
                                                                                                                                                                                                                                                                                            Scyralone dehydratase (Fragment).

Ophiostoma piliferum.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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Ophiostoma piliferum.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Ophiostomataceae; Ophiostomataceae; Ophiostom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Inhibitors and genetic analysis of scytalone dehydratase confirm presence of DHN-melanin pathway in sapstain fungi."; Mycol. Res. 106:1331-1339(2002).
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R; QBNJII; 1-122.
C; GO:0016836; F:hydro-lyase act
C; GO:0006582; F:melanin metabol
nterPro; IPR004235; Scytalone D;
nterPro; TPR004235; Scytalone dh; 1.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.

NCBI_TaxID=150568;
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01-OCT-2002, sequence version 1.
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GG; GO:0006582; P:melanin metabolism; IEA.
InterPro; IPR004235; Scytalone_DH.
Pfam; PF02992; Scytalone_dh; 1.
ProDom; PD022193; Scytalone_DH; 1.
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Fleet C., Breuil C.;
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GO; GO:0016836; F:hydro-lyase activity; IE

GO; GO:0006582; P:melanin metabolism; IEA.

InterPro; IPR004235; Scytalone_DH.

Pfam; PF02982; Scytalone_dh; I
                                                                                                                                                                                                                                                                                      Fleet C., Breuil C.;
"Inhibitors and genetic analysis of scytalone dehydratase
presence of DHN-melanin pathway in sapstain fungi.";
Mycol. Res. 106:1331-1339(2002).
                                                                                                                                     ProDom; PD022193; Scytalone_DH; 1.
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                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Search completed: December 5, 2006, 01:12:59
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AJ575152 Sordaria
U95042 Aspergillus
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AF316575 Ophiostom
D86079 Colletotric
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5 Homo sapi
8 Sequence
0 Homo sapi
8 Homo sapi
6 Homo sapi
4 Homo sapi
3 Sequence
31 Agrobacte
31 Agrobacte
38 Xanthomon

Human DNA

MARC 3387

complete

cds.

PLN 13-NOV-1998

Pyricularia

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DEFINITION
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AY098654
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Best Local Similarity:
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                        432 bp
Ceratocystis pinicola scytalone
AY098654
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                                                                                                                       IlePheGluAspGlyArgGluThrPheGlyAspLys
                                                                                                                                                                            ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg
                                                                                                                                                                                                              GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
                                                                                                                                                                                                                                   ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly
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                                                                                                                                                                                                                                                                                                                                   LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys
                                                                                                         ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA
                                                                                                                                                             GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG
                                                                                                                                                                                                                                                                                                                      CTCCGCACGCAGCATCATCGGCGGCACGCCTGGGAGAAGGTGTCCGAGGACGAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Magnaporthe grisea"
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/db_xref="taxon:148305"
/note="sequence obtained from anamorph Pyricularia
whose telemorphic form is unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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YHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Sdh1"
81. .599
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(SD) gene, partial cds.
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AY098655
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Fleet, C. and Breuil, C.
Direct Submission
                                                                                                                    Ceratocystis resinifera
Eukaryota; Fungi; Ascomycota; Pez
Hypocreomycetidae; Microascales;
                                    Fleet, C. and Breuil, C.
Inhibitors and genetic analysis of scytalone dehydratase
the presence of DHN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
                                                                                                                                                                                                                           Ceratocystis
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/db_xref="taxon:72031"
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                                                                                                                       Pezizomycotina;
es; Microascales
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432 17 0 0

linear ase (SD)

gene, partial PLN 16-JAN-2003

188 64

Sordariomycetes; incertae sedis;

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Ceratocystis pinicola
Ceratocystis pinicola
Ceratocystis pinicola
Eukaryota; Pungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-APR-2002) Wood Science, University Columbia, 4th Floor, 2424 Main Mall, Vancouver, E Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleet, C. and Breuil, C. Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DIM-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)
/translation="EWADWYDSKDWDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
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oin(<1. .69,138. .>432)
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BC V6T1Z4, Canada
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AY214004
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                                                                                                                                                                                   Submitted (08-JAN-2003) Wood Science, University of British Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
                                                                                                                                                                                                                                                                                                                                                                     Ceratocystis resinifera
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Microascales; Microascales incertae sedis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
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Loppnau, P.A.
Direct Submission
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                 <233. .>934
/gene="SD1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="EWADRYDSKDWDRLXRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
 join(<233.
                                                                                                  /organism="Ceratocystis resinifera"
/mol_type="genomic DNA"
/isolate="EL3-21"
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                 4041-2424 Main Mall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/protein_id="AAM34801.1"
/db_xref="GI:21238820"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /specific_host="Pinus contorta"
/db_xref="taxon:95837"
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                                               country="Canada: Alberta, Edson"
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isolate="125-214"
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syctalone dehydratase I (SD1) gene,
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                                                                                                                                                                                                                                                                                                  A scytalone dehydratase gene from Ophiostoma floccosum restores the melanization and pathogenicity phenotypes of a melanin-deficient Colletotrichum lagenarium mutant Mol. Genet. Genomics 266 (1), 126-132 (2001)
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Wang, H. L., Kim, S. H. and Breuil, C.
                                                                                                                                                                                                   Submitted (25-OCT-2000) Wood Science, Columbia, 2424 Main Mall, Vancouver,
                                                                                                                                                                                                                                   2 (bases 1 to 1477)
Wang, H. and Breuil, C.
Direct Submission
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wdrlrrtiaptlridyrsfldklweampaedpikmisdpnvlgdpllktqopfvgasrw
ervsddevvgwhqlrvphqrytdatkttvkvkghahsankhwykkvdgvwkfaglype
irwseydfdkvfasgreefgdedidv"
                                                                                                                                                                              Location/Qualifiers
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join(316. .394,471. .571,635. .1105)
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<316. .>1105
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/gene="OSD1"
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                                                                                                                                                                                                                                                                                                                                      Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant Pathology, Faculty of Agriculture, Kyoto Prefectural University; Shimogamo, Kyoto, Kyoto 606, Japan (E-mail:y_kubo@kpu.ac.jp, Tel:075-702-0957, Fax:075-702-0957)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kubo,Y., Takano,Y., Noriko,E., Yasuda,N., Tajima,S. and Furusawa,I. Cloning and structural analysis of the melanin biosynthesis gene encoding scytalone dehydratase of Colletotrichum lagenarium
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Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
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                                                                                                                /gene="SCD1"
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oin(222
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                                                                                                                                                                                                                                   db_xref="taxon:5462"
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Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostomatales; Ophiostomataceae; Ophi
                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (22-APR-2002) Wood Science, University
Columbia, 4th Floor, 2424 Main Mall, Vancouver,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /db_xref="taxon:61273"
                                                               'gene="SD"
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Ophiostoma piceae
Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
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                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-APR-2002) Wood Science, Universit Columbia, 4th Floor, 2424 Main Mall, Vancouver, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleet, C. and Breuil,
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                                                                                                                          /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADBFIG
MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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join(<1. .69,128. .>423)
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                                                                                                                                                                                                                                                                                         'gene="SD"
                                                                                                                                                                                                                                                                                                                    country="Canada"
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scytalone dehydratase (SD)
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Ophiostoma minus i
partial cds.
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AY098659.1 GI:21:
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2. (bases 1 to 423)
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Ophiostoma setosum gene, partial cds.
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Ophiostoma setosum
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                                                                                                                                                                                                                                                                                                                                         AHSANQHWYRKVDGVWKFAG"
                                                                                                                                                                                                                                                                                                                                                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIV
MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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isolate="NZFS3734"
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="SD"
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oin(<1. .69,128. .>423)
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Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DNN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)
2. (bases 1 to 428)
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Ophiostoma minus
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Ophiostoma minus
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Eukaryota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostomataceae; Ophiostomataceae; Ophiostomataceae; Ophiostomataceae;
              Fleet, C. and Breuil, C.
Inhibitors and genetic analysis of scytalone dehydratase confirm
the presence of DNN-melanin pathway in sapstain fungi
Mycol. Res. 106 (11), 1331-1339 (2002)

(bases 1 to 433)
Fleet, C. and Breuil, C.
Direct Submission
                                                                                                                                                                                                                                                                           partial cds.
                                                                                                                                                                                                                                                                                             Ophiostoma minus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-APR-2002) Wood Science, University Columbia, 4th Floor, 2424 Main Mall, Vancouver, Location/Qualifiers
                                                                                                                                                                                                                                          AY098658.1
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                                                                                                                                  (bases 1 to 433)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
MISDPSVLGNPLLRTQHSFGASRWGRVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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/db_xref="GI::21238828"
/db_xref="GI::21238828"
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/gene="SD"
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/gene="SD"
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country="United Kingdom"
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Wood Science,
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58-4 scytalone dehydratase
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Matches:
Conservative:
Mismatches:
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University of British
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AY098665
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Ophiostoma setosum isolate 160-38
partial cds.
AY098665
                                                                                                                                                                                                                                                                                                                                                          Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleet, C. and Breuil, C. Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)
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Ophiostoma setosum
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Fleet,C. and Breuil,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscarioscario
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MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
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/country="Canada"
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/isolate="160-38"
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/protein_id="AAM34804.1"
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join(<1. .69,128. .>422
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                               product="scytalone dehydratase"
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dehydratase (SD) gene,
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ataceae; Ophiostoma.
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                      Score:
                                        Pred. No.:
                                                       Alignment
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                           of Life and Environmental Science; Nishikawatsu 1060, Matsue, Shimane 690-8504, Japan (B-mail:j-kihara@life.shimane-u.ac.jp, Tel:81-85-32-6597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kihara, J., Moriwaki, A., Ueno, M., Tokunaga, T., Arase, S. and Honda, Y. Cloning, functional analysis and expression of a scytalone dehydratase gene (SCD1) involved in melanin biosynthesis of the phytopathogenic fungus Bipolaris oryzae phytopathogenic fungus Bipolaris oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bipolaris oryzae
Eukaryota; Pungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kihara, J. and Moriwaki, A.
Direct Submission
Submitted (16-JAN-2003) Junichi Kihara,
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                                                                                                                               QLRVPHQRYTDESRATVAVKGHAHSFNTHWYKKI DGEWKFAGLNPDI RWYEYDFDKVF
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                                                                                                                                                                                                                                                         'gene="BSCD1"
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                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
strain="D9/F6-69"
                                                                                                                                                                                                                                                                                                                                                                                     organism="Bipolaris oryzae"
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RESULT 15
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AY098664 414 bp DNA linear PLN 16-JAN Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)
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gene, partial cds.
AY098663
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Ophiostoma piliferum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiosto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)

2. (bases 1 to 414)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 country="United Kingdom"
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isolate="198-2GF"
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1 (bases 1 to 414)
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Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi Mycol. Res. 106 (11), 1331-1339 (2002)
2 (bases 1 to 414)
Fleet, C. and Breuil, C.
Direct. Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada Location/Qualifiers
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AY098664
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AHSANTHWYRKVDGVWKFA"
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join(<1 ..69,120. .>414)
/gene="SD"
/codon_start=1
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/gene="SD"
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|mol_type="genomic DNA"
| isolate="201-1A"
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-Q=/abss/ABSSWEB spool/US10507132/runat_04122006 143523 9593/app_query.fasta_1
-Q=/abss/ABSSWEB spool/US10507132/runat_04122006 143523 9593/app_query.fasta_1
-DB=N Geneseq -QFWT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -STRATT=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss05h
-USER=US10507132 @CGN 1 761 @runat 04122006 14352 9593 -NCPU=6 -ICPU=3
-NORMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-NARN_TIMEOUT=30 -THREADS=1 -XGAPDEX=60 -FGAPDE=60 -FGAPDEXT=7
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Adc16602 Scytalone
Adc16603 Scytalone
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ADC16592
ID ADC16592
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                                                                                                                                                                                                                                    Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; gene; ds.
                                                                                                                                                                                                                                                                                Scytalone dehydrogenase gene #SEQ ID 3.
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 24-FEB-2003; 2003WO-JP001980.
                                                                                                                                                                                                     Magnaporthe grisea.
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                                                               WO2003076628-A1.
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                                                                                                                                                         Location/Qualifiers
                                                                                                           /product= "scytalone dehydrogenase"
/partial
                                                                                           note= "no stop codon"
                                                                                                                                          *tag=
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ABN17793
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AAK73808
ADQ50306
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ABL80052
ACH45193
AAH33155
ABL09311
ADA53154
ABL09310
ABK42692
ADB60848
ADC16597
ADC16596
ADC16601
ABZ49282
ADB249282
ADB249282
ADB0651
AAV13085
ACC71276
ABQ673286
ADU25639
AAH84614
ABC12719
AABN24458
ADN75514
ABN74514
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ACH29653
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AAC74929
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Adc16508 SCDH rela
Adc16501 SCDH rela
Adc16501 SCDH rela
Adc16501 SCDH rela
Abz49282 Human gen
Acd86651 E. coli K
Aav13085 Kylanase
Acf71276 Photorhab
Abg67328 Listeria
Adu25639 cDNA enco
Aah84614 E. coli g
Aac12719 Human sec
Abn24458 Human ORF
Abn74318 Human ORF
Abn24318 Human ORF
Abac13215 Kenopus s
Aac74929 Human ORF
Abn77234 Human ORF
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Abn7736 Cotton ex
Abn17793 Human ORF
Ach95952 Klebsiell
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Abx61362 Arabidops
Aak73808 Human imm
Adq50306 Novel can
Aak59789 Human imm
Aai83543 Human pol
Ach38954 Human foe
Aed94874 Germ cell
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Ab109311 Drosophil
Ada53154 Human cod
Ab109310 Drosophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scytalone
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                                                 IlePheGluAspGlyArgGluThrPheGlyAspLys
                                                                                                              ValTrpLysPheAlaGlyLeuLysProAsplleArgTrpGlyGluPheAspPheAspArg
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                                                                                                                                                       GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC
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ADC16602
ID ADC16602 standard; DNA; 600 BP
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AC ADC16602;
XX
DT 18-DEC-2003 (first entry)
XX
Scytalone dehydrogenase; SCDH;
XX
Magnaporthe grisea.
XX
DS Magnaporthe grisea.
XX
PN W02003076628-A1.
XX
I8-SEP-2003.
XX
PN W02003076628-A1.
XX
I1-MAR-2002; 2002JP-00066955.
XX
YX
Z4-FEB-2003; 2002JP-00066955.
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CT TARAR-2002; 2002JP-00066955.
XX
YX
I1-MAR-2002; 2002JP-00066955.
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PR 12-MAR-2002; 2002JP-00066955.
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I1-MAR-2002; 2002JP-00066955.
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PR 12-MAR-2003; 2003WO-JP001980.
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IN-SEB-2003; 2003WO-JP001980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a gene encoding scytalone dehydrogenase (SCDH), that functions in the presence of an inhibitor, comprising an optionally mutatred, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia
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                                                                                                              MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr
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LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
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RESULT 3
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Best Local Similarity:
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US-10-507-132-4 (1-172)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; gene; ds.
                                                                                                                                                                                                                                                         Sequence 610 BP; 148
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                                                                                                                                                                                                                                                         A; 179 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610
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                                                                                                                                                                                                                                                         113 T;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a gene encoding scytalone dehydrogenase (SCDH that functions in the presence of an inhibitor, comprising an optional mutated, defined amino acid sequence given in the specification. Also disclosed is a method for evaluating rice blast fungus (Pyricularia oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase inhibitors. The gene is useful for screening for new SCDH inhibitors a evaluating sensitivity to them. The current sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding for scytalone dehydrogenase (SCDH), useful for screening for SCDH inhibitors and evaluating sensitivity to them.
                                                                                                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 516 BP; 119 A; 151 C; 155 G; 91 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scytalone dehydrogenase gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; SEQ ID NO 1; 50pp; Japanese.
    Dumas
                                                                                                                                                                                          gene therapy;
                                                                                                                                                                                                                                   Human secreted
                                                                                                                                                                                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                                         AAC19354;
                                                                                                                                                                                                                                                                                                                  AAC19354 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.:
                                                                                  21-FEB-2000;
                                                                                                                                       EP1033401-A2
                                                                                                                                                                 Homo sapiens
                                                       26-FEB-1999;
                             (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                           136 LysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 ThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
                                                                                                                                                                                                                                                                                                                                                                        466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 TCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGAC
  Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 SerGluAspGluVallIeGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                          5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTG
                                                                                                                                                                                                                                                                                                                                                                                      PheAspPheAspArgIlePheGluAspGlyArgGluThrPheGlyAspLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCCGATATCCGCTGGGGCGAG
                                                                                  2000EP-00200610
                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                          chromosome mapping; ss.
                                                                                                                                                                                                                                  protein 5'
                                                        99US-0122487P
                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.21e-97
97.00
100.0%
100.0%
56.4%
  Duclert A,
                                                                                                                                                                                                       sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                  EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1-516)
                                                                                                                                                                                                                                  SEQ ID NO: 23429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative: Mismatches: Indels:
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Matches:
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  Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
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RRESULT 6
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                        Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 375 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression and secretion vectors
                                                                                                                                                                                                                                       Algate PA,
                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000; 2000US-0207484P
                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001WO-US017756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ovarian cancer related cDNA clone SEQ ID NO:3030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL80052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL80052 standard;
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                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAGCTCCAAACAAGTTTTAGGA 370
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                                                                                                                                                                                                                                          Harlocker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 A; 96 C;
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8.00
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                                                                                                                                                                                                                                    SL,
                                                                                                                                                                                                                                          Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 104 T;
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Matches:
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Mismatches:
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Claim 1; SEQ
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NO 3030; 489pp; English.
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hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour CDNA library length gene from a suitable library e.g., a The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypoptide (II) of a ovarian tumour polypoptide encoded by a polypuclectide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide behalf of the patient of the polynucleotide behalf of the polynucleotide of the patient of the polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the amount of polynucleotide behalf of the patient with (IV), detecting the patient of the patient with (IV). using well known techniques

Sequence 405 BP; 127 A; 86 Ç 77 G; 115 T; 0 U; 0 Other;

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DB:
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                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                       Alignment Scores: '
                                                                                                                                                                                                                                                                Local Similarity:
                                                                                                                                                   Human foetal brain cDNA #5918
                                                                                                                                                                13-OCT-2003
                                                                                                                                                                            ACH45193;
                                                                                                                                                                                       ACH45193 standard; cDNA; 512
                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                            70
                                                                                                                                                                                                                GTGAGCTCCAAACAAGTTTTAGGA 134
                                                                                                                                                                                                                      ValSerSerLysGlnValLeuGly 77
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                         37.9
8.00
100.0%
100.0%
4.7%
                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                rength:
                                                                                                                                                                                                                                                   0 0 0 8 405
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Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

17-APR-2003. US2003073623-A1

30-JUL-2001; 2001US-00918995

30-JUL-2001; 2001US-00918995

(DRMA/) DRMANAC R T. LABAT I.

(STAC/) (LABA/) STACHE-CRAIN DICKSON M C. JONES L W. Φ

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58

New polynucleotide sequences obtained from various cDNA libraries, useful

antisense DNA or RNA. as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating

Claim 1; SEQ ID NO 32405; 44pp; English

identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences seqdata.uspto.gov/sequence.html?DocID=20030073623 are useful in diagnostics as expressed sequence tags (EST) The invention relates to an isolated polynucleotide comprising any one 38043 CDNA sequences, appearing as ACH12789-ACH50831, whose sequence was 엺

Sequence 512 BP; 145 A; 119 C; 103 G; 133 Ŧ; 0 U; 12 Other;

맑 S AAH33155 RESULT Query Match: Best Local Similarity: Alignment Scores: US-10-507-132-4 (1-172) x ACH45193 (1-512) Percent Similarity: NO.: 440 GTGAGCTCCAAACAAGTTTTAGGA 463 70 ValSerSerLysGlnValLeuGly 77 47.4 8.00 100.0% 100.0% 4.7% Indels: Mismatches: Conservative: Matches: ength: 512 0 0

AAH33155 standard; cDNA; 1521

03-SEP-2001 (first entry)

Human colon cancer antigen encoding cDNA SEQ ID NO:211.

colorectal carcinoma; Human; colon cancer; colon cancer antigen; diagnosis; detection; 88

WO200122920-A2

05-APR-2001

28-SEP-2000; 2000WO-US026524.

29-SEP-1999; 03-NOV-1999; 99US-0157137P 99US-0163280P

(HUMA-) HUMAN GENOME SCI INC

SM, Barash sc, Birse B Rosen

WPI; 2001-235357/24. P-PSDB; AAG73724.

Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

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New isolated nucleic acid
genes from Drosophila and
detection reagent for detecting 1000 for elucidating cell signaling and ce
                             or more
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The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of

(REAS-) RES

HELIX RES INST.
RES ASSOC BIOTECHNOLOGY.

Otsuki T, Wakamatsu A, Sato H, Ii Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y;

Ishii S; Tamechika

Н;

diseases

in

RESULT 9
ABLO93111
ID ABLO
XX ABLO
XX ABLO
XX Dros
DE Dros
XX Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Pred. No.: CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where the CC proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene therapy CC and vaccine production. N and P may be used in the prevention, diagnosis CC cancelle, N and P may be used to treat disorders associated with diagnosis color cancer antigens to the color cancer associated with inappropriate P expression. For CC example, N and P may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of P by expressing inactive proteins or to complement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids control a host cell and culturing the cell to express the proteins. N and P CC can be used in the prevention, diagnosis and treatment of colorectal CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent CC pages 666 to 682 and page 7053 of the sequence listing were missing at CC time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922 US-10-507-132-4 (1-172) Drosophila; developmental pharmaceutical; gene; ss. Sequence 1521 BP; 411 A; Claim 1; 23-MAR-2000; 2000US-0191637P 11-JUL-2000; 2000US-00614150 WO200171042-A2 Drosophila melanogaster. Drosophila ABL09311 standard; cDNA; 1690 BP No.: Venter JC, 23-MAR-2001; 2001WO-US009231 27-SEP-2001. 26-MAR-2002 (first entry) ABL09311; (PEKE) PE CORP NY. Scores: 2001-656860/75. DB; ABB65208. 310 70 ValSerSerLysGlnValLeuGly 77 Page 2354; 9803pp; English GTGAGCTCCAAACAAGTTTTAGGA 333 melanogaster expressed polynucleotide SEQ ID NO 22415 Adams M, gene; 135 8.00 100.0% 100.0% 4.7% × AAH33155 匚 355 C; PWD, biology; cell signalling; insecticide (1-1521) Myers 380 Mismatches: Indels: Matches: Conservative: Length: G; 371 Η, 0 1521 8 0 0 0 U; 4 Other; RESULT 1
ADDAS3154
ADDAS3154
ADDAS3154
AC ADDA
AC ADDA
AC ADDT 20AC ADD AC ADDAS 밁 Ś Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic; Gene Therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease; gene; ss. New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for disease which the gene is involved, or as target molecules for gene therapy. Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T, Homo sapiens Human coding sequence, 20-NOV-2003 Claim 1; SEQ ID NO 722; 205pp; English. WPI; 2003-395539/38. P-PSDB; ADA54793. 14-SEP-2001; 2001JP-00328381. 24-JAN-2002; 2002US-0350435P. 21-MAR-2002; 2002EP-00006586. 19-MAR-2003 ADA53154;

(first entry)

SEQ ID

722.

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Score:

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Alignment & Pred. No.:
                                                                                                                                                                         Best Local Similarity:
Query Match:
DB:
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                                                                                                                                        US-10-507-132-4 (1-172) x ABL09311 (1-1690)
                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016176). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                     Sequence 1690 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
ADA53154 standard; cDNA; 2002
                                                                      1040 AAAGTTATAGCTCCGACTCTGAGA 1063
                                                                                                                                                                                                                                                                                      Scores:
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                                                                                          LysValIleAlaProThrLeuArg 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 22415; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                     611 A; 335 C;
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Matches:
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                                      Alignment Scores: Pred. No.:
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                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
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P-PSDB; ABB65207.
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                                                                                          Sequence 4182 BP;
                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 22412; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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 Length:
Matches:
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DB:
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US-10-507-132-4 (1-172)
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Human; connective tissue related disorder; cancer; gene therapy; cytostatic; gene; ds.
                                                        Genomic sequence
                                                                                                                                                               ABK42692 standard; DNA; 12822 BP
                                                                                        21-MAY-2002 (first entry)
                                                                                                                                                                                                                                   1714 AAAGTTATAGCTCCGACTCTGAGA 1691
                                                                                                                                                                                                                                                              40 LysVallleAlaProThrLeuArg 47
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#591 encoding novel human connective tissue polypeptide.

WO200155343-A1

07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 07-JUL-2000; 07-JUL-2000; 31-JAN-2000; 04-FEB-2000; 19-MAY-2000; 17-JAN-2001; 2001WO-US001322 02-MAR-2000; 2000US-0216647P. 2000US-0216880P. 2000US-021748PP. 2000US-0217496P. 2000US-0218290P. 2000US-0220963P. 2000US-0180628P 2000US-0184664P 2000US-0209467P. 2000US-0205515P 2000US-0198123P

30-AUG-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 23-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 2000US-0225447P 2000US-0225747P 2000US-0225758P 2000US-0225758P 2000US-0225759P 2000US-0226681P 2000US-022668P 2000US-0226868P 2000US-0227182P 2000US-0227108P 2000US-0227099 2000US-0229344P 2000US-0229344P 2000US-0229344P 2000US-0225214P. 2000US-0225266P. 2000US-0225267P. 2000US-0225268P. 2000US-0224518P. 2000US-0224519P. 2000US-0225213P.

2000US-0220964P

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06-SEP-2000
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2000US-0232080P
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2000US-0231968P
2000US-0232397P
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2000US-0232399P
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2000US-0232400P
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2000US-0230438P.
2000US-0231243P.
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2000US-0231244P.
2000US-0231414P.
 2000US-0233064P
2000US-0234274P
2000US-0234274P
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2000US-023499P
2000US-0235836P
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2000US-0247967P
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RESULT 13
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU8635-AAU86923) and the polynucleotide (cDNA and genomic) sequences (AAU86435-AAU86923) and the polynucleotide invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                           Connective tissue related genomic DNA #591.
                                                      04-DEC-2003
                                                                              ADB60848;
                                                                                                     ADB60848 standard;
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2000US-0249297P

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cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;

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2000US-022934P. 2000US-022934P. 2000US-022934P. 2000US-022934F. 2000US-022934SP. 2000US-022951P. 2000US-023943P. 2000US-023043P. 2000US-023043P. 2000US-0231242P. 2000US-0231244P. 2000US-0231244P. 2000US-0231244P.	2000US-0214880P. 2000US-021749FP. 2000US-0211496P. 2000US-0211496P. 2000US-0221963P. 2000US-022964P. 2000US-0225213P. 2000US-0225214P. 2000US-0225266P. 2000US-022526PP. 2000US-0225268P. 2000US-022547P. 2000US-022547P. 2000US-022549P. 2000US-022549P. 2000US-022549P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022546P. 2000US-022575P.	A1. 2002US-00092154. 2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-018974P. 2000US-01893P. 2000US-0198123P. 2000US-0205515P. 2000US-0209467P. 2000US-0214866P. 2000US-02158135P.	antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic; antiarteriosclerotic; immunosuppressive; antirheumatic; dermatological; nephrotopic; virucide; fungicide; antibacterial; antiparasitic; gene therapy; ds; connective tissues disorder; rheumatoid arthritis; systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer; cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; cardiovascular disease; atherosclerosis; myocarditis; cardiopulmonary bypass complication; autoimmune disease; multiple sclerosis; allergic reaction; asthma; rhinitis; eczema; inflammatory condition; Crobn's disease; nephritis; gastrointestinal disorder; inflammatory bowel disease; nephritis; organ transplant rejection; immune system disorder; Bruton's disease; X-linked lymphoproliferative syndrome; B-cell lymphoproliferative disorder; HIV; AIDS; infection; chromosome identification; chromosome mapping; connective tissue related polynucleotide; gene; ds.
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08-DEC-2000;
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08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 tissue-related polynucleotide encoding connective tissue antigens (CTA). The polypeptide or polynucleotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polypeptides, polynucleotides and antibodies are particularly useful for treating, preventing and/or prognosing disorders of connective tissues (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus, scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g. alherosclerosis, myocarditis or cardiopulmonary bypass (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
                                                                                                                                                                                                                                                                                                                                                                                               complications), autoimmume uiscussifications, autoimmume uiscussifications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New connective tissue-related polypeptides and polynucleotides, useful for treating, preventing and/or prognosing e.g. disorders of connective tissue. (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 1579; 248pp; English
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neoplasias
                 primer; ss
                                Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; PCR,
                                                            SCDH related primer #SEQ ID
                                                                                        18-DEC-2003
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                                      KUMIAI CHEM IND CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                               e encoding for scytalone dehydrogenase (SCDH), useful for screening SCDH inhibitors and evaluating sensitivity to them.
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Search completed: December 4, 2006, 23:59:43 Job time: 591 secs

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Sequence Sequence Sequence

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Result
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-MODEL=frame+_p2n.model
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-LOOPEXT=0 -UNITS=51ts -STRATF=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALICN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss07
-USER=US10507132_@CGN_1 1 204_@runat_04122006_143535_9709 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -MAIT_DSPELOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARM_TIMEOUT=30 -THEADS=1 -XGAPDEX=60 -FGAPDEXT=7
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/EMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*
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                                    Sequence 23429, A
Sequence 722, App
Sequence 14178, A
Sequence 13845, A
Sequence 12371, A
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             Sequence
Sequence
            23, Appl
25, Appl
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Alignment Scores
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SEQ ID NO 23429
LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/513,999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                        OTHER INFORMATION: m=a
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NAME/KEY: misc_feature
LOCATION: 14
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US-09-489-039A-1757
US-09-513-999C-1332
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US-09-949-016-26290
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US-09-280-116-93
US-09-280-118-93
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US-09-949-016-1937
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US-09-949-016-2882
                                                                                                                                                                                                                                                                                              Sequence Tags and Encoded Human Proteins.
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Sequence

93, Appl
3, Appl
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5281, Ap
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2, Appli 2882, Ap 5, Appli 7, Appli 4055, Ap 1, Appli

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143766, 169814

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103519, 118088, 118089,

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16794, A 9687, Ap 24969, Ap 1757, Ap 3332, Ap 115423, A 115423, A 26290, A 38776, A

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RESULT 3
US-09-949-016-14178
; Sequence 14178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAGAHARI, KENJI

APPLICANT: MASUHO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA

FILE REFERENCE: 084335/0160

CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: 60/350,435

PRIOR FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: JP 2001-328381

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 3381

SOFTWARE: PACENTIN VET. 2.1

SEQ ID NO 722

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Query Match:
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Best Local Similarity:
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Patent No. 6979557
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ORGANISM: Homo sapiens
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WAKAMATSU, AI
SATO, HIROYUKI
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
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YAMAMOTO, JUN-I
ISONO, YUUKO
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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Best Local Similarity:
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US-09-949-016-13845
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-10-09-08
PRIOR FILING DATE: 2000-10-09-08
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-09-08
PRIOR FILING DATE: 2000-10-09-08
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PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14178
LENGTH: 88266
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SEQ ID NO 13845
LENGTH: 152132
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FULL REFERENCE: CL001307

CURRENT FAPHICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20
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95 ValSerGluAspGluValIleGly 102
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Best Local Similarity:
US-10-507-132-4 (1-172) x US-09-189-060B-23 (1-166)
                                                                                                                                Pred. No.:
                                                                                                                                                    Alignment Scores:
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APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method Of Providing No. 62
FILE REFERENCE: 4772.204-US
CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
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; ORGANISM: Human
US-09-949-016-12371
                                                                                                                                                                                          US-09-189-060B-23
                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23
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Patent No. 6812339
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APPLICANT: Dalboge, Henrik
APPLICANT: Sandal, Thomas
APPLICANT: Kauppinen, Mark
APPLICANT: Borge, Diderich
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                        LENGTH: 166
TYPE: DNA
ORGANISM: Hybrid
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US-09-189-060B-25/c
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                                                       Score
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                                                                                                                            US-09-711-164-242
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Forsyth, R. Allyn
APPLICANT: Obleso, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 242, Application US/09711164 Patent No. 6589738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 25
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                                                                                                                                                                                                                                                                                             FILE REFERENCE: ELITEA.008A
CURRENT APPLICATION NUMBER: US/09/711,164
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-9
NUMBER OF TO TO THE
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APPLICANT: Sandal, Thomas
APPLICANT: Kauppinen, Markus
APPLICANT: Borge, Diderichsen
TITLE OF INVENTION: Method Of Providing No.
FILE REFERENCE: 4772.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/189,060B
CURRENT FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/DK97/00216
PRIOR FILING DATE: 1997-05-12
NUMBER OF SEQ ID NOS: 74
                                                                                                                                           ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(297)
                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 181
                                                                                                                                                                                                                               ENGTH:
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RESULT 9
US-09-513-999C-16794
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; ORGANISM: Homo sapiens
US-09-513-999C-16794
US-10-507-132-4 (1-172) x US-09-270-767-9687 (1-377)
                                                   Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                   Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 16794
LENGTH: 303
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16794, Application US/09513999C Patent No. 6783961
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                             TYPE: DNA ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                       LENGTH: 377
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Best Local Similarity:
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                   US-09-513-999C-3332/c
                                        RESULT 13
                                                                                                                                                          US-10-507-132-4 (1-172) x US-09-489-039A-1757 (1-399)
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILLY ONLY ON THE COURSE OF THE PRICE OF THE COURSENT STATE COURSENT STATE ON THE COURSENT STATE ON THE COURSE OF THE COURSE OF THE COURSE OF THE ONE OF SEQ ID NO 1757
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR THING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1757
LENGTH: 399
THENGTH: 399
THENGTH: 399
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LENGTH: 377
TYPE: DNA
ORGANISM: Drosophila melanogaster
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Sequence 3332, Application US/09513999C
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
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                                                                                                                      140 GlyValTrpLysPheAlaGly 146
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                                                                                3 GGCGTGTGGAAGTTCGCCGGC 23
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Conservative:
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3332

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. Patent No. 6783961
FILE REFERENCE: 59.US2.REG

APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.

Patent No. 6783961

INFORMATION:

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Best Local Similarity:
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    Percent Similarity:
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                                                                           US-09-621-976-15423
                                                                                                                                                                                                                                                                                Sequence 15423, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15423
                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                     LENGTH: 479
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                        343 ATGGTGTCCTCCAAACAAGTA 323
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Patent No. 6783961

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

Patent No. 6783961

FILLE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION STATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 1132
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              Search completed: December 4, 2006, 18:39:27
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Best Local Similarity:
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US-09-513-999C-1132/c
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Job time : 221 secs
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                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 488
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: 331..486
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                                                                                      94 LysValSerGluAspGluVal 100
                                                                  AAGGTGTCGGAAGATGAAGTT 381
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US-09-513-999C-3332

NAME/KEY: UNSURE LOCATION: 74 OTHER INFORMATION: Xaa=Asp or

Gly

NAME/KEY: misc_feature LOCATION: 450 -OTHER INFORMATION: r=a NAME/KEY: misc_feature LOCATION: 150. OTHER INFORMATION: b=c

or g or

NAME/KEY: CDS . LOCATION: 230..463

FEATURE:

TYPE: DNA
ORGANISM: Homo sapiens

ENGTH: 463

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Minimum
Maximum
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Perfect score:
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-DB=-Published Applications NA Wain -QFWT=fastap -SUFFIX=011p2n.rnpbm
-MINMATCH=0.1 -LOOPEXT=0 -UNITS-bits -START=1 -RND=-1 -MATRIX=011go
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODR=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-MAXLEN-20000000000 -HOST-abssoch
-I 134 @runat 04122006 143539 9762 -NCPU=6 -ICPU=3
-NO RR-USIN-200000000 -THESOCO 1 1 1334 @runat 04122006 143539 9762 -NCPU=6 -ICPU=3
-NO RWAP -NEG SCORES=0 -WAIT -DSPBLOCK-100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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seq length: 2000000000
                                                                                                                                                                            Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US007_PUBCOMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US008_PUBCOMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US009A_PUBCOMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US009A_PUBCOMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US009C_PUBCOMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*

16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Ygapop 60.
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                                 Description
 Sequence 3030, Ap
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                                                                      Sequence 3030, Application US/09867701

Retent No. US20020132237A1

REPRICANT: Notes Paul A.

REPLICANT: Aglate, Paul A.

REPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3030

LENGTH: 405

TYPE: DNA

ORGANISM: Homo sapien

US-09-867-701-3030
                               Alignment Scores:
Pred. No.:
                     Score:
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 Percent Similarity:
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US-10-106-698-221

US-10-106-698-221

US-10-301-480-36243

US-10-301-480-36243

US-10-301-480-649652

US-10-301-480-649652

US-10-301-480-649653

US-10-027-632-53712

US-10-027-632-53712

US-10-027-632-53712

US-10-027-632-53712

US-10-027-632-53712

US-10-027-632-53712

US-11-060-756-118545

US-11-060-756-123173

US-11-060-756-123173

US-11-060-756-223123

US-11-075-859-11216

US-11-175-859-11216

US-11-175-859-11216

US-10-741-600-48623

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               Length:
Matches:
 Conservative:
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Sequence 321, App
Sequence 36244, A
Sequence 36244, A
Sequence 649652,
Sequence 649653,
Sequence 11206, A
Sequence 1579, Ap
Sequence 1579, Ap
Sequence 53712, A
Sequence 53712, A
Sequence 51712, A
Sequence 11872,
Sequence 11875,
Sequence 11875,
Sequence 11875,
Sequence 11875,
Sequence 11875,
Sequence 11875,
Sequence 206628,
Sequence 206628,
Sequence 211216, Ap
Sequence 28918, A
Sequence 28918, A
Sequence 11917, A
Sequence 11917, A
Sequence 34632, A
Sequence 48622, A
Sequence 48622, A
Sequence 48623, A
Sequence 48633, A
Sequence 48633, A
Sequence 48635, A
Sequence 33837, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 141, App
Sequence 215, App
Sequence 242, App
Sequence 23467, A
Sequence 23467, A
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Sequence 110025, Sequence 141, Ap

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CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIN version 3.1
SEQ ID NO 49239
LENGTH: 600
TYPE: DNA
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DB:
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32405
LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32405, Application US/09918995
publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: HOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIERARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Sequence 49239, Application US/10972079 Publication No. US20050153317A1
                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                         APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
                                                                                                                                                                        TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEE! TITLE OF INVENTION: LIVESTOCK FILE REFERENCE: MMI1110-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...($12)
OTHER INFORMATION: n = A,T,C
 ORGANISM: Chicken
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ROSENFELD, David
KERR, Richard
BATES, Stephen
HOLM, Tom
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LENGTH: 1521
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-507-132-4 (1-172)
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CURRENT APPLICATION NUMBER: US/10/106,698

CURRENT APPLICATION NUMBER: US/20/26524

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR PILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                Sequence 11207, Application US/11097143 Publication No. US20050208558A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20 GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                        560 CTTAGAAAGGTCATTGCTCCCACA 537
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US-10-301-480-36244; Sequence 36244, Application US/10301480; Publication No. US20060057564A1
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: in the Human Genome FILE REFERENCE; 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
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PRIOR FILLING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILLING DATE: 2000-02-24
PRIOR FILLING DATE: 2000-03-23
NUMBER: 60/191,637
PRIOR FILLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36243
LENCTH: 1877
TYPE: DNA
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36243, Application US/10301480 Publication No. US20060057564A1
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PRIOR FILING DATE: 1999-11-12
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TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FASTSQ for Windows Version 4.0
SEQ ID NO 36244
LENGTH: 1877
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RESULT
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapien US-10-301-480-649652
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NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 649652
LENGTH: 1877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                     542 CTTAGAATTGATTACAGATCTTTC 565
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; Sequence 649653, Application US/10301480

US-10-301-480-649653

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CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 649653
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Best Local Similarity:
Query Match:
; TYPE: DNA; ORGANISM: Homo sapiens US-10-094-749-722
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US-10-094-749-722
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US-10-301-480-649653
                                                                                ; APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
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                                                  SEQ ID NO 722
LENGTH: 2002
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APPLICANT: SUGIYAM
APPLICANT: OTSUKI,
APPLICANT: WAKAMAT
APPLICANT: SATO, H
APPLICANT: ISHII,
APPLICANT: ISHII,
APPLICANT: YAMAMOT
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TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
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NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHII
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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YAMAMOTO, JUN-ICHI
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5. US20030219741A1
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Percent Similarity:
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US-09-764-847-1579
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PRIOR FILLING DATE: 1999-10-05
PRIOR PELLOATION NUMBER: 60/160,191
PRIOR FILLING DATE: 1999-10-19
PRIOR FILLING DATE: 1999-10-29
PRIOR FILLING DATE: 1999-10-28
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-12
PRIOR FILLING DATE: 1999-11-28
PRIOR FILLING DATE: 1999-11-28
PRIOR FILLING DATE: 1999-12-28
PRIOR FILLING DATE: 1999-12-28
              Sequence 1579, Application US/09764847
PATENT NO. US20020132767A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11206, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
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FILE REFERENCE: PC009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4182
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US-10-027-632-53712/c
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Best Local Similarity:
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US-10-092-154-1579
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Best Local Similarity:
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US-09-764-847-1579
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                                                                                                                     Sequence 53712, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC009C1
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CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2001-01-17
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TYPE: DNA
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TYPE: DNA
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NAME/KEY: misc_feature; LOCATION: (1)...(715517); OTHER INFORMATION: n = A US-10-027-632-53712
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Best Local Similarity:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SEQ ID NO 53712
LENGTH: 715517
                                                                                                                                                                  SOFTWARE: FastSEQ
SEQ ID NO 53712
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/185,218
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TYPE: DNA
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NAME/KNY: misc feature
LOCATION: (1)...(715517)
OTHER INFORMATION: n = A,T,C or
                                                                                                  TYPE: DNA
ORGANISM: Human
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1: ZMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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US-10-507-132-15

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Sequence 3, Appli
Sequence 13, Appl
Sequence 16, Appl
Sequence 15, Appl
Sequence 14, Appl
Sequence 18, Appl
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US-10-507-132-13
; Sequence 13, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
   APPLICANT: KOICHITO KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION UNUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
   PRIOR APPLICATION NUMBER: US/10/507,132
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
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                                                               Query Match:
DB:
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                                          US-10-507-132-4 (1-172) x US-10-507-132-13 (1-600)
                                                                                      Percent Similarity:
Best Local Similarity:
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; LENGTH: 600
; TYPE: DNA
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SEQ ID NO 16
LENGTH: 610
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RESULT 3
US-10-507-132-16
; Sequence 16, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
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; ORGANISM: Pyricularia oryzae
US-10-507-132-16
                                                                                                                                                            US-10-507-132-4 (1-172) x US-10-507-132-16 (1-610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOICHITO KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
NUMBER OF SEQ ID NOS: 19
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                                                                              ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG
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LENGTH: 538
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TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-02586PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR PILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Pyricularia
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VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
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CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 545
TYPE: DNA
ORGANISM: Pyricularia oryzae
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US-10-507-132-14
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Sequence 14, Application US/10507132
Publication US/20060223136A1
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APPLICANT: KOICHITO KAKU et al.
APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
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                                 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
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; LENCTH: 729
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
US-10-507-132-18
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APPLICANT: KOICHAYO KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE 'TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
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Publication No. US20060223136A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                   CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC
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APPLICANT: KOICHITO KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0258PUS1
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 732
TYPE: DNA
ORGANISM: Pyricularia oryzae
US-10-507-132-17
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Best Local Similarity:
Query Match:
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US-10-507-132-17
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Publication No. US20060223136A1
GENERAL INFORMATION:
           Sequence 1, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:
APPLICANT: KOICHIYO: KAKU et al.
TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING ITITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
FILE REFERENCE: 1254-0256PUS3
CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER:
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APPLICANT: HARKIN, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
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Query Match:
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LENGTH: 516
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NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
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LOCATION: (1)..(516)
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ORGANISM: Pyricularia oryzae
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PatentIn
                       SEQ ID NOS: 483996
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Matches:
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APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
ITILE OF INVENTION: MUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105493.4
PRIOR APPLICATION NUMBER: EP 04105493.4
PRIOR APPLICATION NUMBER: EP 04105493.9
PRIOR APPLICATION NUMBER: EP 04105495.9
PRIOR APPLICATION NUMBER: EP 04105496.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo Sapiens
US-11-266-748A-184560
                                                                                                                                 Percent Similarity:
Best Local Similarity:
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US-11-266-748A-71004
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                                                           US-10-507-132-4 (1-172) x US-11-266-748A-71004 (1-926)
                                                                                                                Query Match:
                                                                                                                                                                                                          Alignment Scores:
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LENGTH: 497
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 71004
                                                                                                                                                                                                                                                               FEATURE: misc feature LOCATION: (144)...(446) OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                         No.:
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GTGAGCTCCAAACAAGTTTTAGGA 775

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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: (481)...(783)
OTHER INFORMATION: n is a,
US-11-266-748A-123815
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US-11-266-748A-123815/c
; Sequence 123815, Application US/11266748A
; Publication No. US20060134663A1
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Best Local Similarity:
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Publication No. US20060141495A1
GENERAL INFORMATION:
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
                     APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: MCLAird, Paul L.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Corn.
FILE REFERENCE: 38-21 (53660)B
FULL REFERENCE: 38-21 (53660)B
FULL REPLICATION NUMBER: US 60/606,880
PRIOR APPLICATION NUMBER: US 60/606,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harkin, Paul
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; NUMBER OF SEQ ID NOS: 25043
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4533
LENGTH: 1586
TYPE: DNA
ORGANISM: Zea mays
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; ORGANISM: Homo Sapiens
US-11-266-748A-32509
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                                                                 US-10-507-132-4 (1-172) x US-11-266-748A-32509 (1-3304)
                                                                                                                    Query Match:
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                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 
SEQ ID NO 32509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REPERENCE: 55815-0102 (31918) CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT FILING DATE: 2005-11-03 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                               LENGTH: 3304
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                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/662,276
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 812 GTGAGCTCCAAACAAGTTTTAGGA 835
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CURRENT APPLICATION NUMBER: US/10/507,132
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: JP 2002-66955
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 21
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US-10-507-132-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-507-132-4 (1-172) x US-11-218-305-16760 (1-4322)
                                                    US-10-507-132-4 (1-172) x US-10-507-132-8 (1-21)
                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized primer US-10-507-132-8
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Sequence 8, Application US/10507132

Publication No. US20060223136A1

GENERAL INFORMATION:

APPLICANT: KOICHITO KAKU et al.

TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT

FILE REFERENCE: 1254-02588US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 16760
LENGTH: 4322
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Publication No. US20060141495A1
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CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping TITLE OF INVENTION: Corn. FILE REFERENCE: 38-21 (53660)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: MCLAIRT, Paul L.
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Search completed: December 4, 2006, 17:46:42 Job time: 173 secs

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Result
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-Q=/Abss/ABSWEB spool/US10507132/runat_04122006 143531 9655/app_query.fasta 1
-DB=EST -QFMT=fastap -SUFFIX=01ip2n rst -MINMAYCH=0.1 -TOOPCL=0 -TOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=01ig0 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss07
-USER=US10507132 @CGN 1 1 6323 @runat 04122006 143531 9655 -NCPU=6 -ICPU=3
-NORMAP -NEG SCORES=0 -WAIT -DSPBLOCK=102006 143531 9655 -NCPU=6 -ICPU=3
-NORMAP -NEG SCORES=0 -WAIT -DSPBLOCK=102006 143531 9655 -NCPU=120
-WARN TIMEOUT=30 -THHEADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Ygapext 60.0
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  BM863356
BM864194
BM863315
BM864156
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                                                                                                                                                             SUMMARIES
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3305.198 Million cell updates/sec
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BM863356 mgcm006x0
BM864194 mgcm008xJ
BM863315 mgcm006xE
BM864156 mgcm008xD
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04247 ZMMBBb	G90	12	\vdash	4.7	80	45
86247 BP6862	68624	w	æ	٠	8	44
N476575 altr207	47657	9	8	٠	9	43
781295 OC_E	129	13	S	٠	9	42
V027321 ZM_BFb0	V0273	10	ω	٠	9	41
97015 OC_Ba0	Z69701	13	7	٠	9	40
71348 BY <u>47</u> 13	47134	4.	\mathbf{L}	٠	9	39
95673 GR Ea	09567	œ	ຫ	٠	9	38
P100008 BP100008	000	ω	6	•	9	37
G280255 c2b06np.	8025	N	7		11	36
09916 VD0	Q109	w	7		14	35
75905 T143B012	D27590	თ	8		17	34
5566 T143B012	556	ហ	ū	٠	17	ω G
75940 T143B015	275	σı	ω		17	32
75678 T143B007	75	σ	0		17	31
73332 T143B019	273	v	9	٠	17	30
74144 T143B040	274	ភ	N		17	29
76416 T143E	276	ហ	7	٠	17	28
28671 mgcm(28	4.	ω		35	27
5038 mgmt(ü	4	9	2	55	26
63213 mgcm	BM863213	w	æ	٥.	55	25
35120	ū	4	æ		55	24
87183	2	ω	4		71	23
D034317	D034	4.	7	ω	74	22
36729	36	4	4	ω	74	21
63209	w	w	N	9.	85	20
61796 mgcm00	2	ω	\mathbf{r}	9.	85	19
63558 mg	3	w	0		91	18
M863546 mg	53	w	9	N	91	17
64820 mg	2	w	æ	σ	96	16
61952	61	w	9	5	96	15
63340 mc	63	w	4		101	14
64053 mgcm00	2	w	σ	9	102	13
63499 mgcm(53	w	0		104	12
64472	M864	ω	0		106	11
64018 mgcmC	54	w	7	٥.	115	10
63639 mgcm0	63	ω	æ		125	9
M863710 mgcm007	M863	ω	J	5	129	8
64467 mgcm010	M864	ω	643	76.7	132	7
63357 mgcm00	633	ω	w	٥.	w	σ
374 mgcm006	ω ω	w	\vdash	٥.	w	ຫ

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ALIGNMENTS

	JOURNAL COMMENT	TITLE	AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	RESULT 1 BM863356
Contact: Ebbole DJ Department of Plant Pathology & Microbiology Department of Plant Pathology & Microbiology Texas A&M University Peterson Bldg, MS2132, College Station, TX 77843-2132, USA Tel: 979 845 4831 Fax: 979 845 6483 Email: d-ebbole@tamu.edu Chromatogram file of this sequence is available, see contact Chromatogram file of this sequence is available, SCYD_MAGGR SCYtalone	9718ea Unpublished (2002) On Mar 7, 2002 this sequence version replaced gi:19231038.	Bhatteral, K. and Dean, K.A. Expressed sequence tags from the rice blast fungus, Magnaporthe	Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,	Eukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.	Magnaporthe grisea	Magnaporthe grisea (anamorph: Pyricularia grisea)		BM863356.2 GI:30391591	grisea cDNA clone mgcm006x003 5', mRNA sequence. BM863356	619 bp mkNA linear EST 06-MAY-2003 mgcm006x003f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe	

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 161
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                                                                                                  LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
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                                                                                                                                                                                            IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
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IlePheGluAspGlyArgGluThrPheGlyAspLys 172
                                                     ValTrpLysPneAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
                                                                                                                                                                       ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Wector: pBluescriptsK-; Site_1: EcoRI, Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/sex="Mat1-2 hermaphrodite"
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/strain="Guyll"
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US-10-507-132-4 (1-172) x BM864194 (1-657)
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Fax: 979 845 6483
Faxi: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...365 e-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
On Mar 7, 2002 this
Contact: Ebbole DJ
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                                                                                                                                                                                                                                              /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/strain="Guy11"
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MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                 Unpublished (2002)
On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                                                  Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|18TD|...364 e-100
PCR PRimers
                                                                                                                                                                                                                                    Texas A&M University
Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 664)
Ebboole, D. J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
Bhatterai, K. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                  BACKWARD: T7 primer
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                                                                                                                                      FORWARD: T3 primer
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                                                                                   primer: T3.
                                                                                                    mgcm006
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/strain="Guy11"
                                                     1. .664
                                                                 Location/Qualifiers
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ACCESSION VERSION

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ביייייטאטטעז.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xD02 5', mRNA sequence.
BM864156.2 GI:30390915
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/note="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5 reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector segs."
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/cell_type="mycelium"
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Best Local Similarity:
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Peterson Bldg, MS2132, College Station, TX 77843-2132,
Tel: 979 845 4831
Fax: 979 845 6483
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Chromatogram file of this sequence is available,
person;Best nr hit (April. 22, 2003) sp|P56221|SC
dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87
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On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
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Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACKWARD: T7 primer Plate: mgcm008 row: Seq primer: T3.
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{\tt MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr}
                                                                         VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
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/note="Vector: pBluescriptSK: Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
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sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sor
Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see conta
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR
dehydratase >gi|1127197|pdb|1STD|...276 le-73
PCR_PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ Department of Plant Pathology & Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
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                      /clore lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Magnaporthe grisea"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:148305"
/clone="mgcm006xC10"
/sex="Mat1-2 hermaphrodite"
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                                                                                                           Unpublished (2002)
Contact: Ebbole DJ
Contact: Ebbole DJ
Department of Plant Pathology &
Texas A&M University
Peterson Bldg, MS2132, College &
Tel: 979 845 4831
Fax: 979 845 6483
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                             Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >9i|1127197|pdb|18TD|. . . 276 1e-73
PCR. PRimers
                                                                                                                                                                                                                                                                                                                                                   Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
                                                                                                                                                                                                                                                Expressed sequence
                                                                                                                                                                                                                                                              Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; So:
Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                      BM863357.1 GI:19231039
 BACKWARD:
                   FORWARD:
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T3 primer
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Seq primer: T3.
Magnaporthe
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/note=Tvector: pBluescriptsKr; Site_1: EcoRI; Site_2:

XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
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/sex="Mat1-2 hermaphrodite"
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Magnaporthe grisea CM Uni-Zap XR Library
one mgcm010xH12 5', mRNA sequence.
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grisea (anamorph:

Pyricularia grisea)

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Peterson Bldg, MS2132, College Station, TX 77843-2132,
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
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On Mar 7, 2002 this sequence version replace
Contact: Bbbole DJ
Department of Plant Pathology & Microbiology
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Seq primer: T3.
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PCR PRimers
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                        MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr
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(bases 1 to 643)
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/cell type="mycellum"
/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK: Site1: EcoRI; Site2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
where a full-length alignment to the M. grisea genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/mol_type="mRNA"
/strain="Guyll"
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Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
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Ser row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person; Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scy
dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from the rice blast fungus, Magnaporthe
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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             /note="vector: pBluescriptsK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5 reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
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clone="mgcm007xE24"
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/strain="Guy11"
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                                                                            Peterson Bldg, MS2132, College Station, TX 77843
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, person;Best nr hit (April. 22, 2003) sp|P56221|Su
dehydratase >9i|1127197|pdb|1STD|... 293 5e-79
PCR PRImers
                                                                                                                                                                                On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ Department of Plant Pathology & Microbiology Texas A&M University College Station, TX 77
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Magnaporthe grisea
Magnaporthe grisea
Eukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 486)
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486 bp mRNA linear EST 06-MAY-2003 mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm007xG13 5', mRNA sequence.
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                                                    FORWARD: T3 primer
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/clone="Vector: pBluescriptSK-; Site 1: EcoRI; Site 2:
XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5 reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/mol_type="mRNA"
/strain="Guy11"
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/sex="Mat1-2 hermaphrodite"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson Bldg, MS2132, College
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
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On Mar 7, 2002 this sequence version replace Contact: Ebbole DJ

Department of Plant Pathology & Microbiology Texas A&M University

Texas A&M University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed sequence tags from the rice blast fungus, Magnaporthe
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                                                                                     MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
                                                                                                                                                        VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
                                                                                                                                                                                                                                                                                                          MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet
LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal
                                                                                                                                                                                                                                  ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys
                                                                                                                                  ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
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                                                          primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cione lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site 1: EcoR1; Site 2:
XhoI; Unidirectional cloning. EcoR1 side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
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/cell_type="mycelium"
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VERSION
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   US-10-507-132-4 (1-172)
                                                                                                                                  Pred. No.:
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACKWARD: T7 primer
Plate: mgcm010 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
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Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
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                                                                                                                                                                                                                                                                                                       /sex="Mat1-2 hermaphrodite"

/cell type="mycelium"

/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"

/clone lib="Magnaporthe grisea CM Uni-Zap XR Library"

/clone libe "Magnaporthe grisea CM Uni-Zap XR Library"

/note="Vector: pBluescriptSK.; Site_1: EcoRI; Site_2:

XhoI; Unidirectional cloning: EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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/mol type="mRNA"
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x BM864472
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Matches:
Conservative:
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CM Uni-Zap XR Library Magnaporthe
mRNA sequence.
                                                       gi:19232154.
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Score:

ORIGIN

Alignment

No.:

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RESULT 12
BM863499
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grisea
Unpublished (2002)
Unpublished (2002)
On Mar 7, 2002 this sequence version replaced
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
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Magnaporthe grisea
Magnaporthe grisea
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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                                                                                                                                                                                                                                                                                                     Plate:
                                                                                                                                                                                                                                                                                                                                                                                Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
Chromatogram file of this sequence is available, see contact
person;Best nr hit (Aprill 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...260 7e-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                             FORWARD: T3 primer BACKWARD: T7 prime:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Bhatterai, K. and Dean, R.A.
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                                                                                                                                                                                                                                                                                            mgcm006 row
/clone="mgcm006xL19"
/sex="Mat1-2 hermaphrodite"
/sex="Mat1-2 hermaphrodite"
/cell type="mycellum"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI, Site_2:
/note="Vector: pBluescriptSK-; Site_1: EcoRI, Site_2:
XhoI, Unidirectional cloning, EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
                                                                                                                                                                                                                                                 1. .504
                                                                                                                                                                 db_xref="taxon:148305"
                                                                                                                                                                                        /strain="Guy11"
                                                                                                                                                                                                        organism="Magnaporthe grisea"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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SOURCE ORGANISM

KEYWORDS

VERSION ACCESSION DEFINITION

REFERENCE

RESULT 13 BM864053

맑 δ 밁 Ś 밁 Ś 맑 Ş 밁 S 맑 Ş

JOURNAL COMMENT

Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr hit (April. 22, 2003) pdb|45TD|A Chain A, High
Resolution Structures Of Scytalone Dehy. . . 223 6e-58

TITLE AUTHORS

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US-10-507-132-4 (1-172) x BM863499 (1-504)
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                                                                                                                                                                                                                                 Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Eukaryota; Fungi; Ascomycota; Magnaporthaceae; Magnaporthe.
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366 bp mRNA linear EST 06-MAY-2003 mgcm008xM18f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xM18 5', mRNA sequence.
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Peterson Bldg, MS2132,
Tel: 979 845 4831
Fax: 979 845 6483
                                                                          Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
                                                                                                                    Unpublished (2002)
                                                                                                                                                                              Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.
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                                                           Texas A&M University
                                                                                                                                                         Expressed sequence tags from the
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                                                                                                                                                                                                                        (bases 1 to 366)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at room temperature, 150 rpm, harvested, blended,
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104.00
100.0%
100.0%
60.5%
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                                      Station, TX 77843-2132,
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RESULT 14
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Best Local Similarity:
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                                                       KEYWORDS
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                                                                                       649 bp mRNA linear EST 06-MAY-2003 mgcm006xK09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xK09 5', mRNA sequence.
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Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                          BM863340.2 GI:30391603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAla 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="mgcm008xM18"
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/cell_type="mycelium"
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reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person;Best nr htt (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
dehydratase >gi|1127197|pdb|1STD|...361 5e-99
PCR PRimers
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Expressed sequence tags from the rice blast fungus, Mag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: mgcm006 row:
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Mar 7, 2002 this
Contact: Ebbole DJ
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                                                                                                  SerLysGlnValLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg
                                                                                                                                                                                           SerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSer
                     TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
                                                                                                                                                             TCCTTCCTCGACAAGCTCTGGGAGGCAATGCCCGGCCGAGGAGTTCGTCGGCATGGTCTCG
TGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGCTCCCGCACCAG
                                                                              AGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCACTTCATCGGCGCACGCGC
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XhoI; Unidirectional cloning. EcoRI side has T3 primer and
predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days
at room temperature, 150 rpm, harvested, blended,
reinoculated into complete medium 24 h, room temperature,
150 rpm. Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."
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/clone_lib="Magnaport
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2002)
On Mar 7, 2002 this sequence version replaced Contact: Ebbole DJ
Department of Plant Pathology & Microbiology Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77 Tel: 979 845 4831
Fax: 979 845 6483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mgcm001xL17f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm001xL17 5', mRNA sequence.

BM861952
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Magnaporthe grisea
Magnaporthe grisea
Eukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|...209 7e-54
PCR_PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
Expressed sequence tags from the rice blast fungus, Magnaporthe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: d-ebbole@tamu.edu
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XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert.
Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
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             LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSer
                                                                 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr
                                                                                                                 VallleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla
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                                                                                                 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG
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Search completed: December 4, 2006, 18:35:44
Job time : 4369 secs

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